

FIG 1

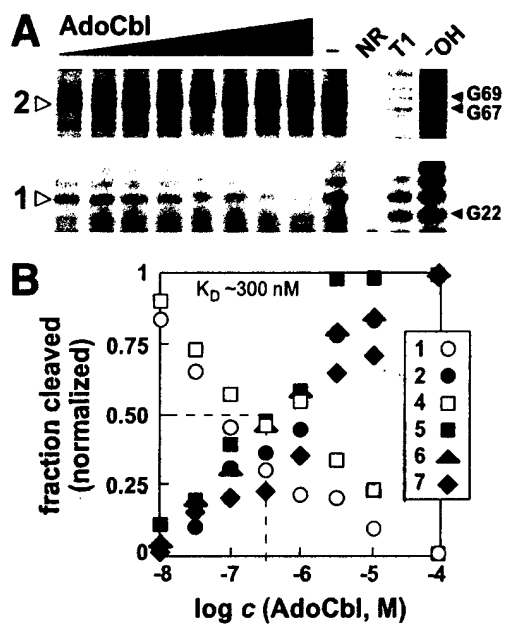


FIG 2

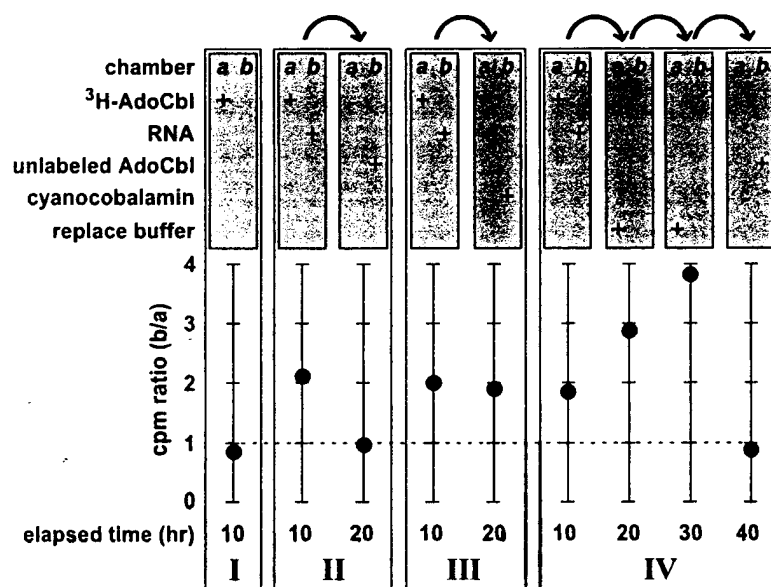


FIG 3

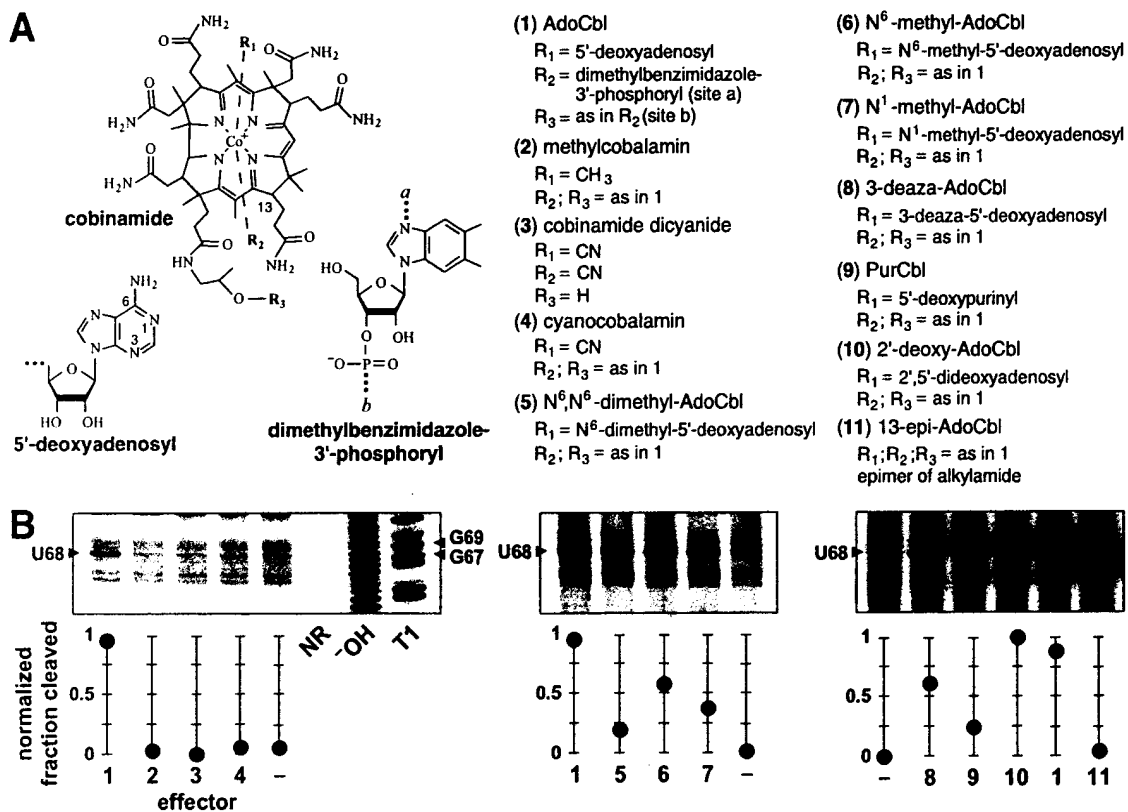


FIG 4

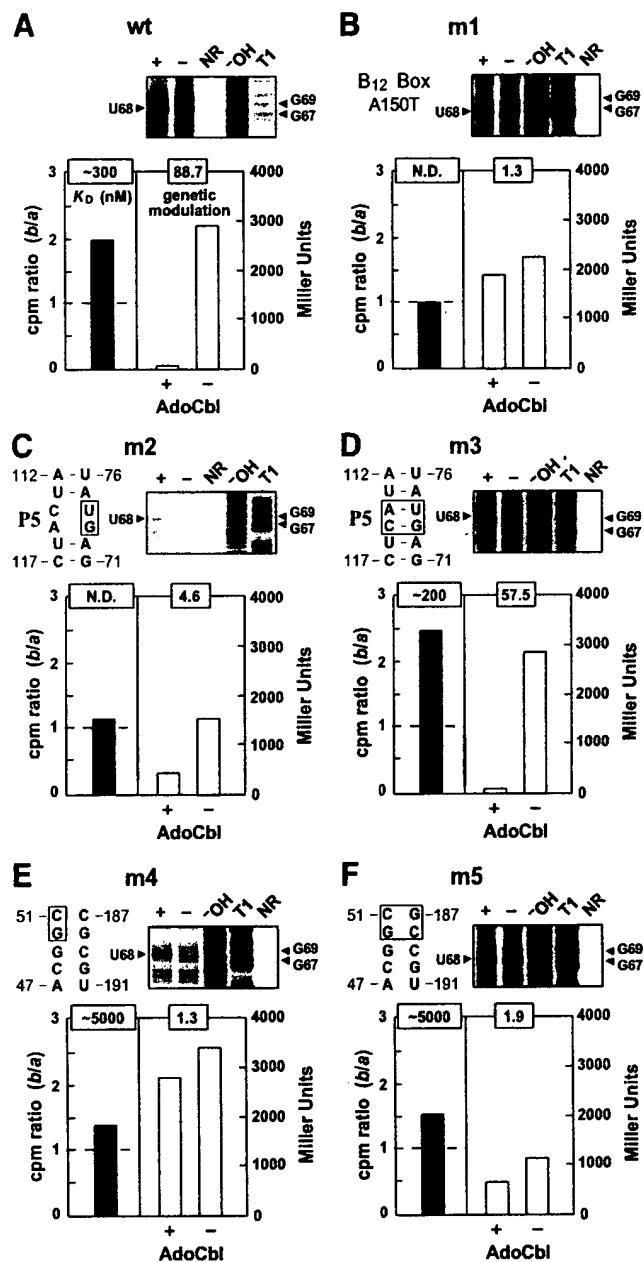


FIG 5

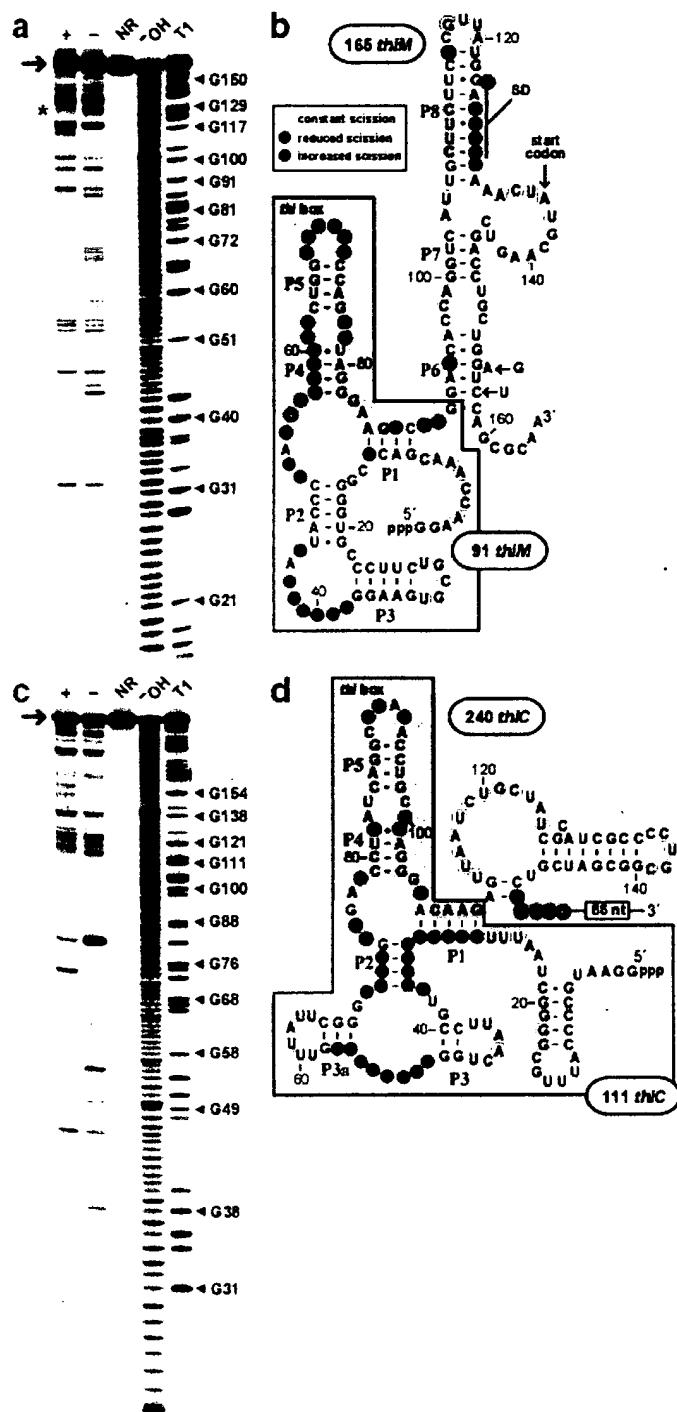


FIG 6

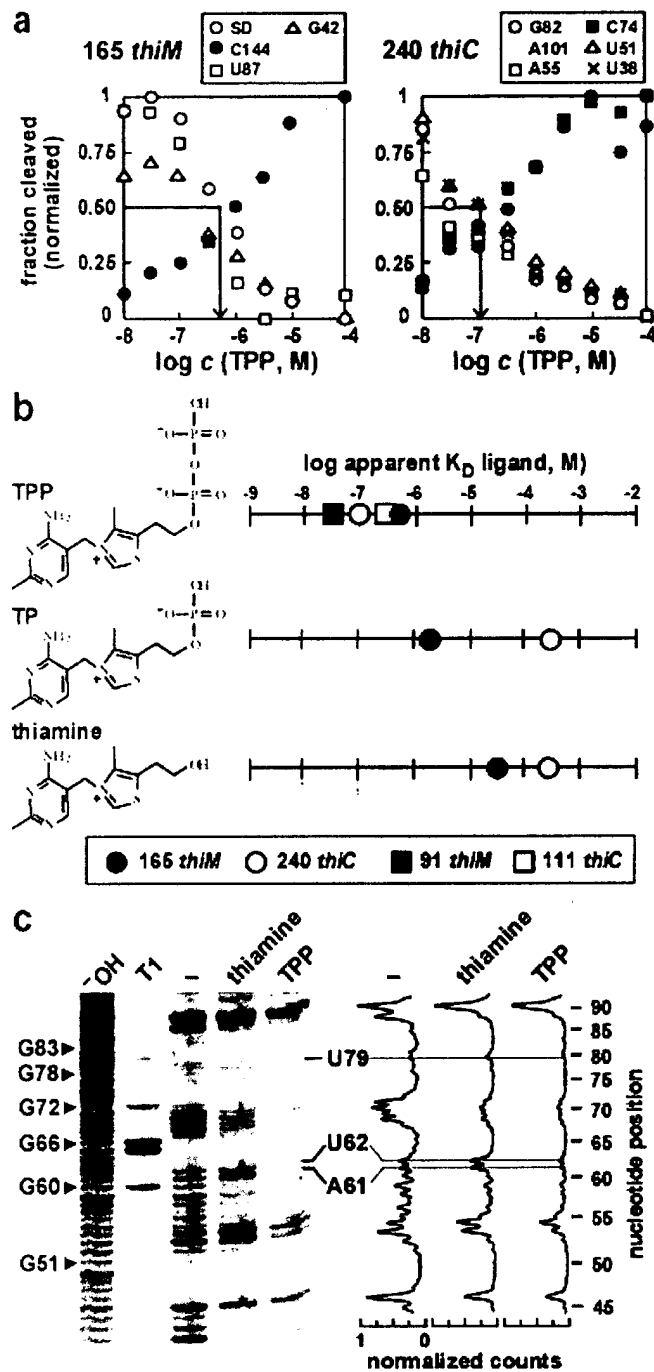


FIG 7

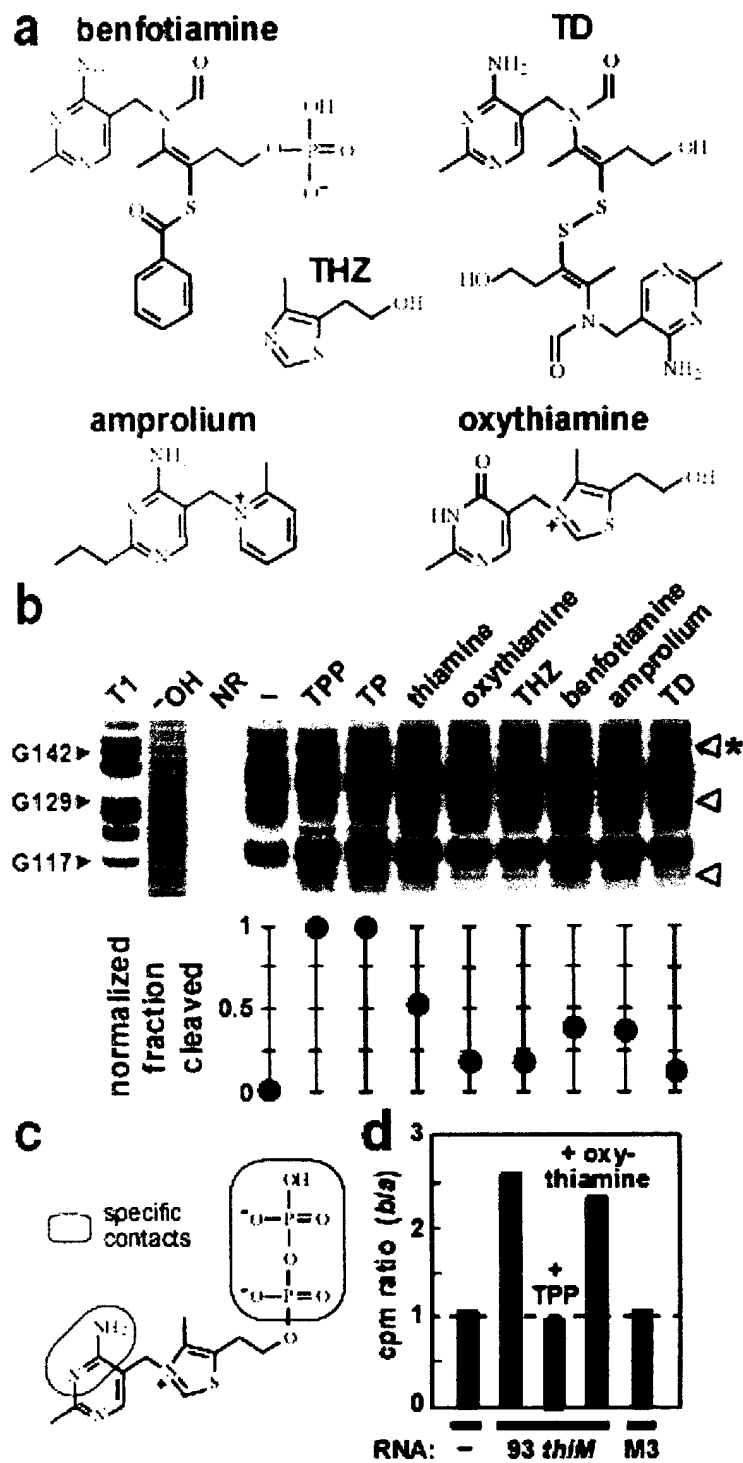


FIG 8

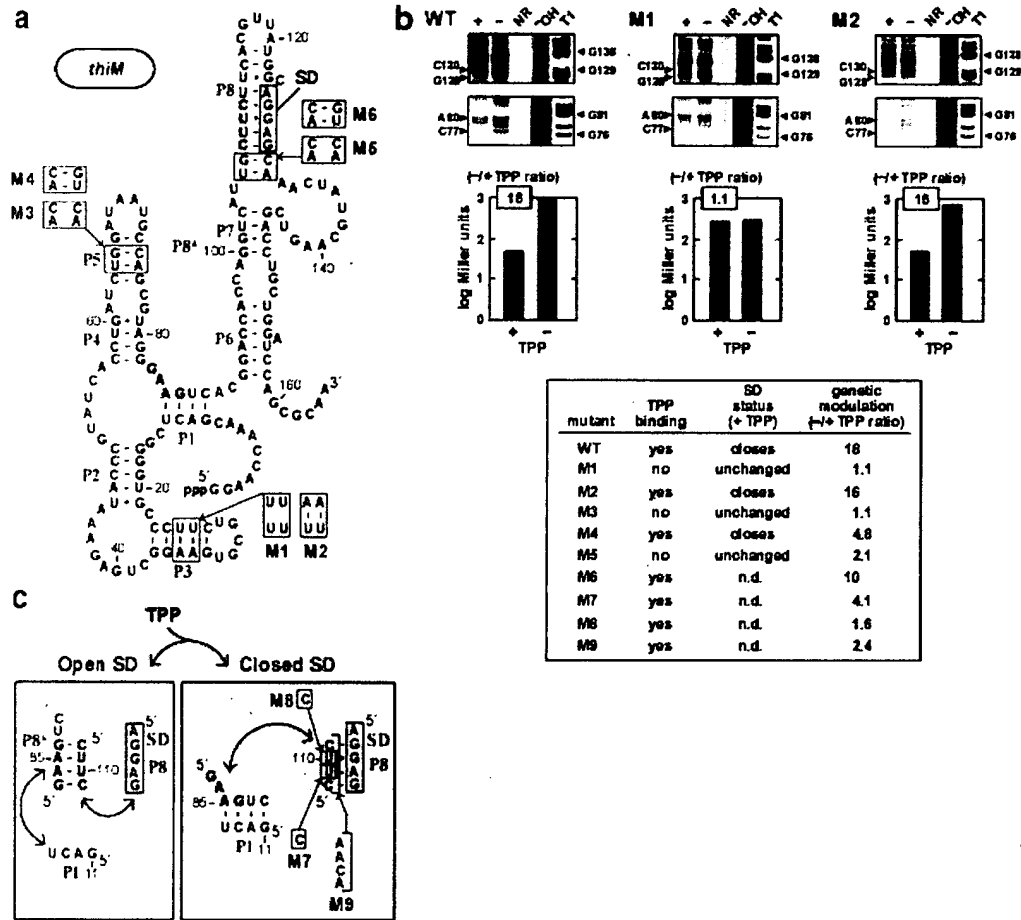


FIG 9

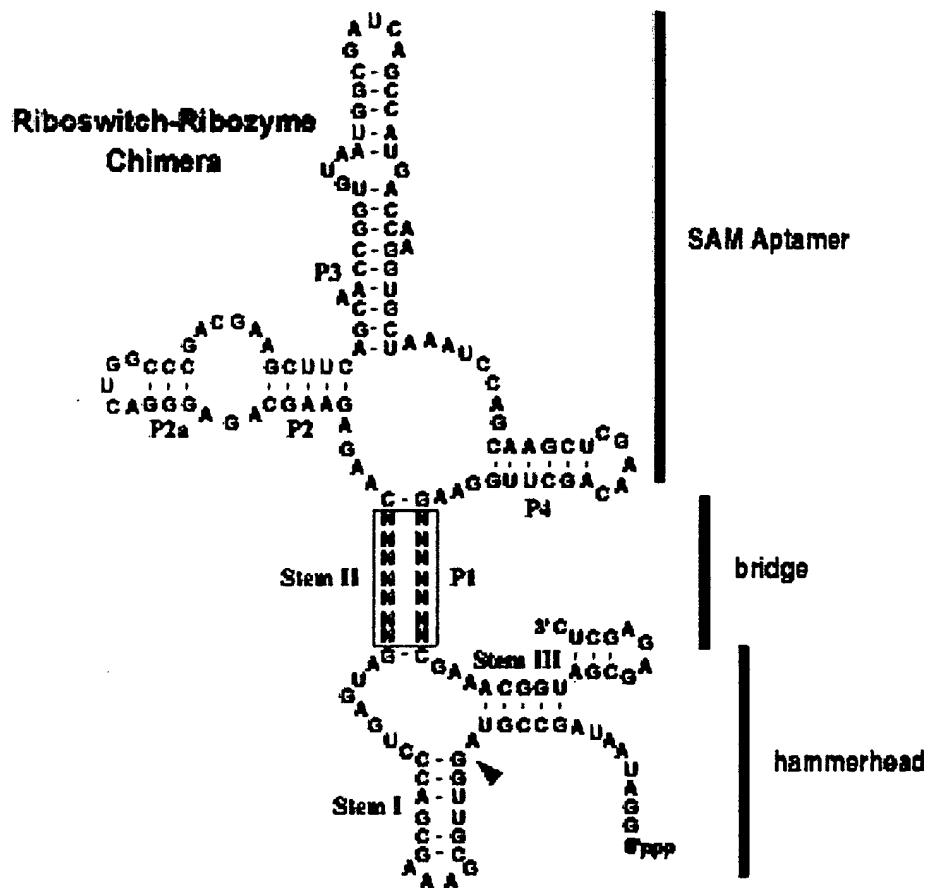


FIG 10

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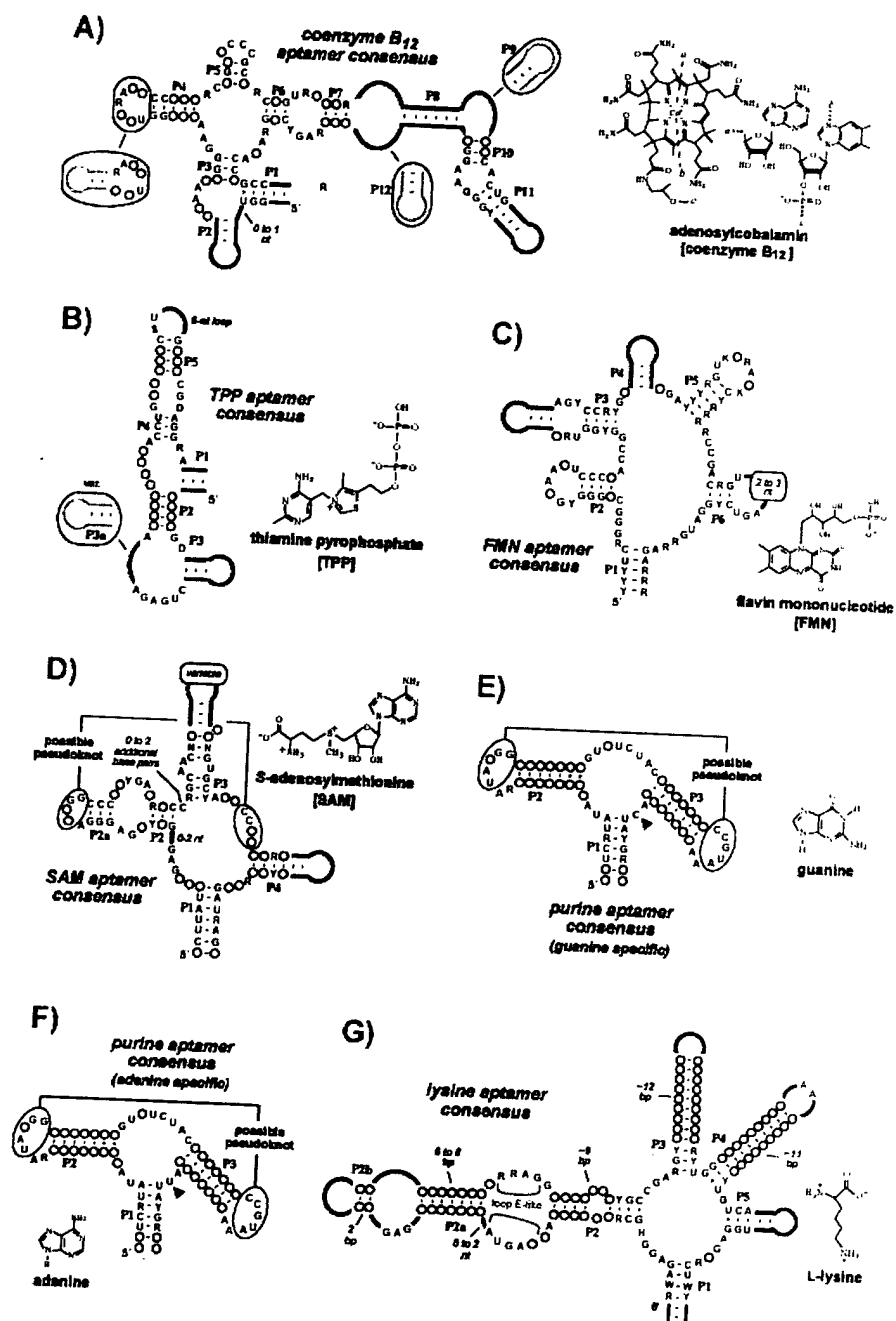


FIG 11

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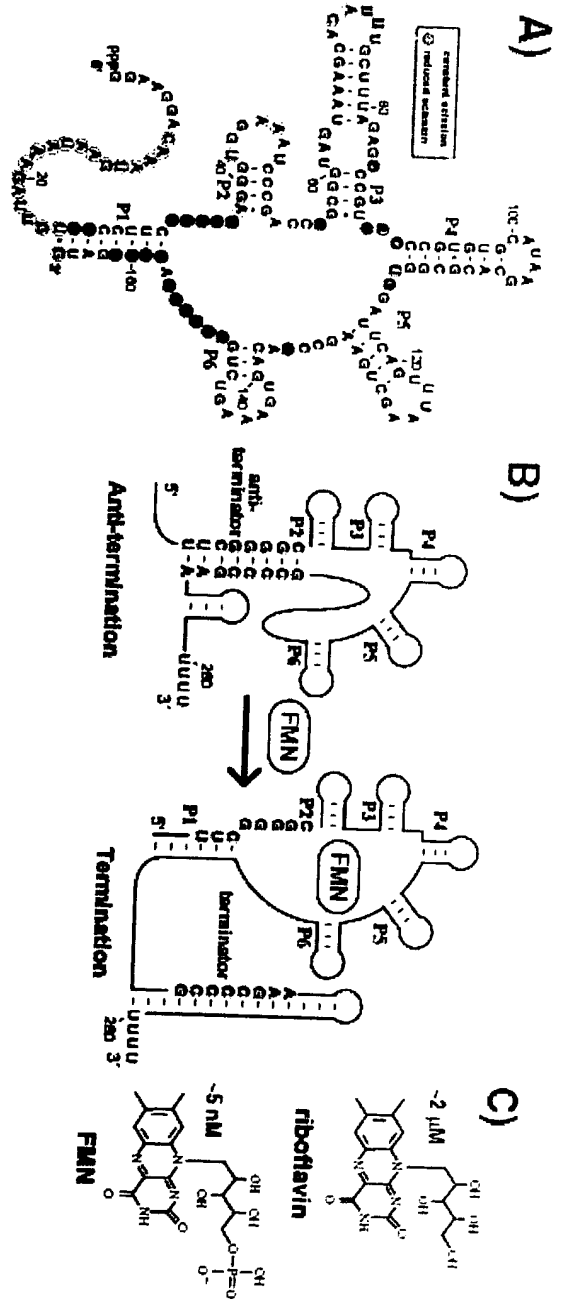


FIG. 12

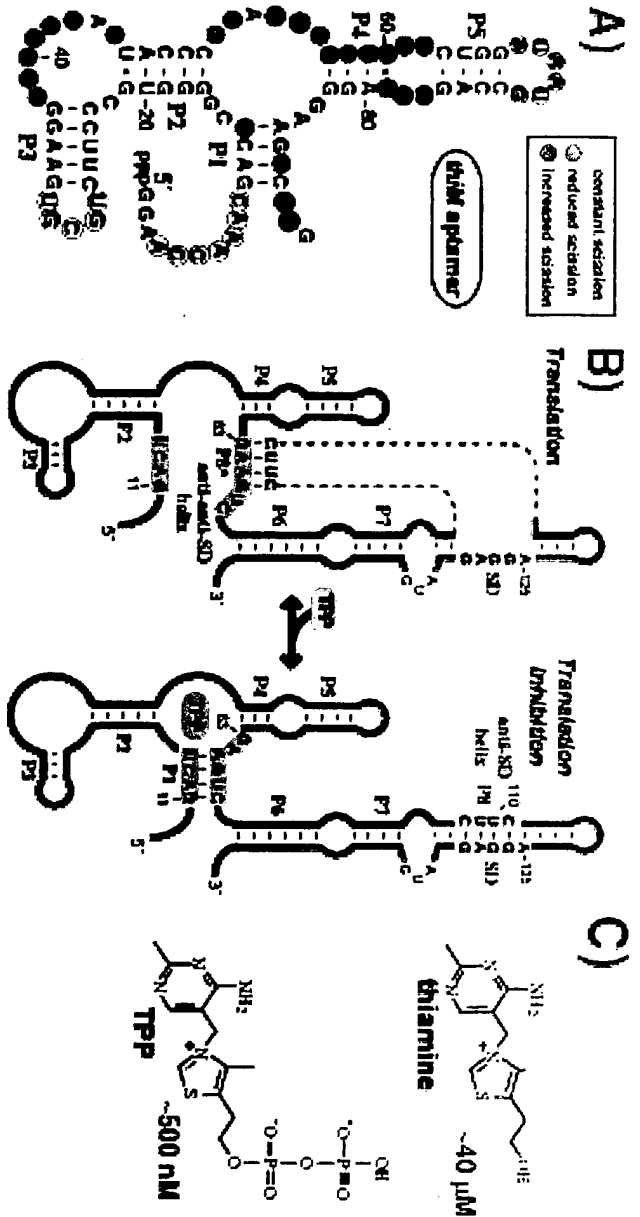


FIG. 13

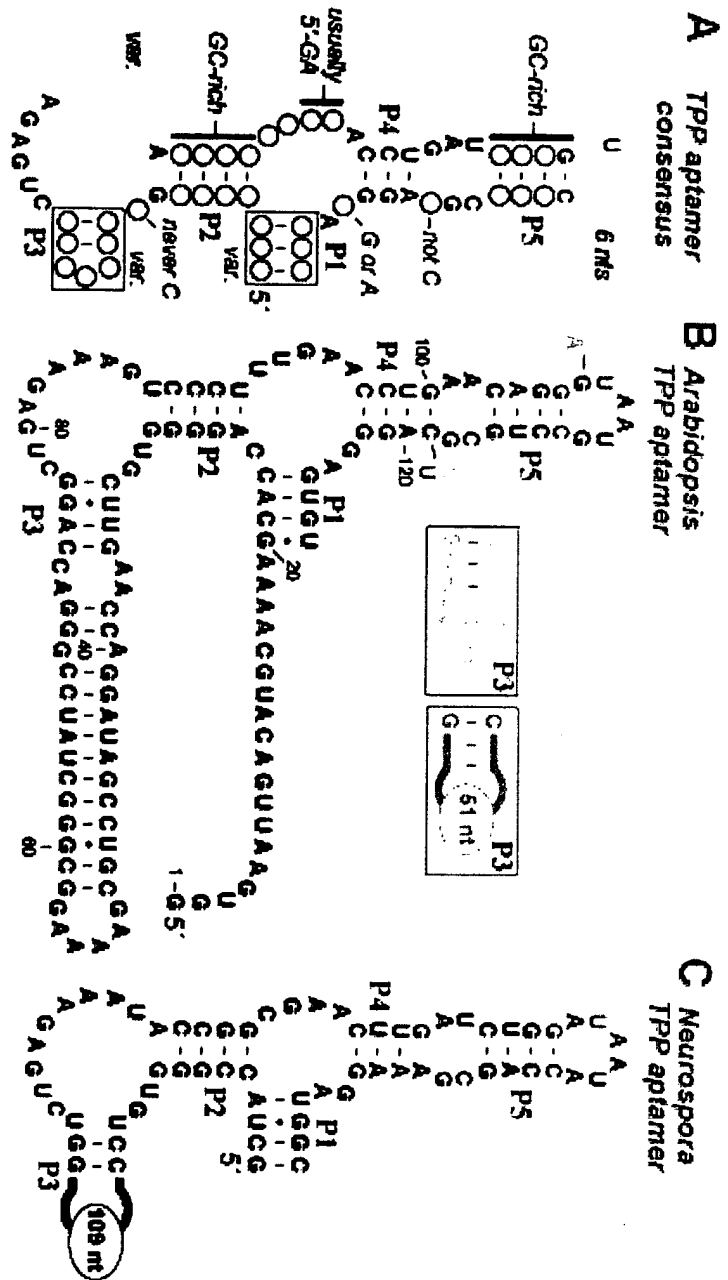


FIG. 14

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Title:
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ID	Position	Accession	Sequence Name	Gene	Location
Bco1	-	2189379	NC_000913.1	Escherichia coli K12 complete genome	thiM operon
Bco2	-	4193775	NC_000913.1	Escherichia coli K12 complete genome	thiC operon
Cac	-	3156195	NC_003030.1	Clostridium acetobutylicum ATCC824 complete genome	thiC
Ncr	+	664	AY007661.1	Neurospora crassa thiamine biosynthesis protein nmt-1 gene	nmt-1
Aor	+	622	AF217509.1	Aspergillus oryzae putative thiazole synthase (thiA) gene	thiA [thi4]
Pox	+	2156	AB033416.1	Fusarium oxysporum sti35 gene for stress-responsive gene product	sti35 [thi4]
Pso	+	461	M93642.1	Fusarium solani STI35 protein gene	sti35 [thi4]
Ath	-	78516	AC005406.3	Arabidopsis thaliana chromosome 2 clone T27A16 map mi54	thiamine gene [thiC]
Pse	+	2296	AF264021.1	Posa securda putative thiamine biosynthesis protein ThiC mRNA	putative thiC
Osa	-	91318	AC084406.7	Oryza sativa chromosome 3 BAC OSJNBa0067E01 genomic sequence	putative thiC

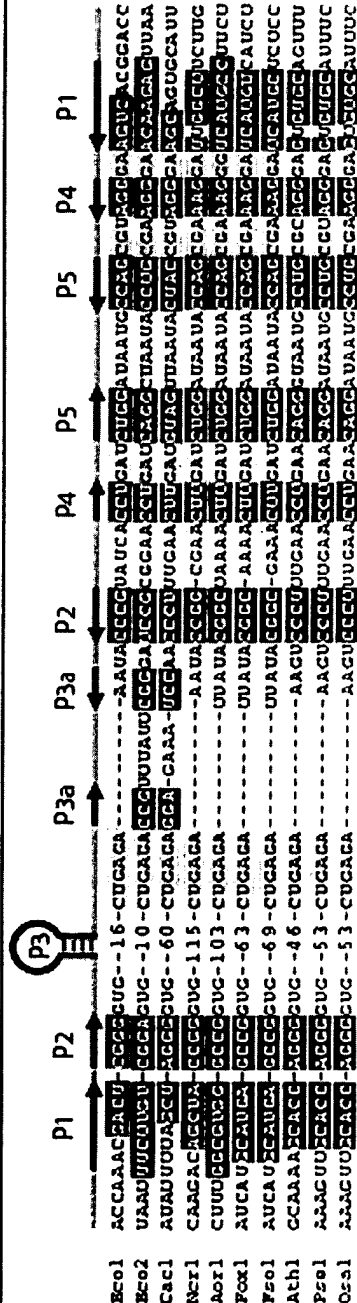


FIG 15

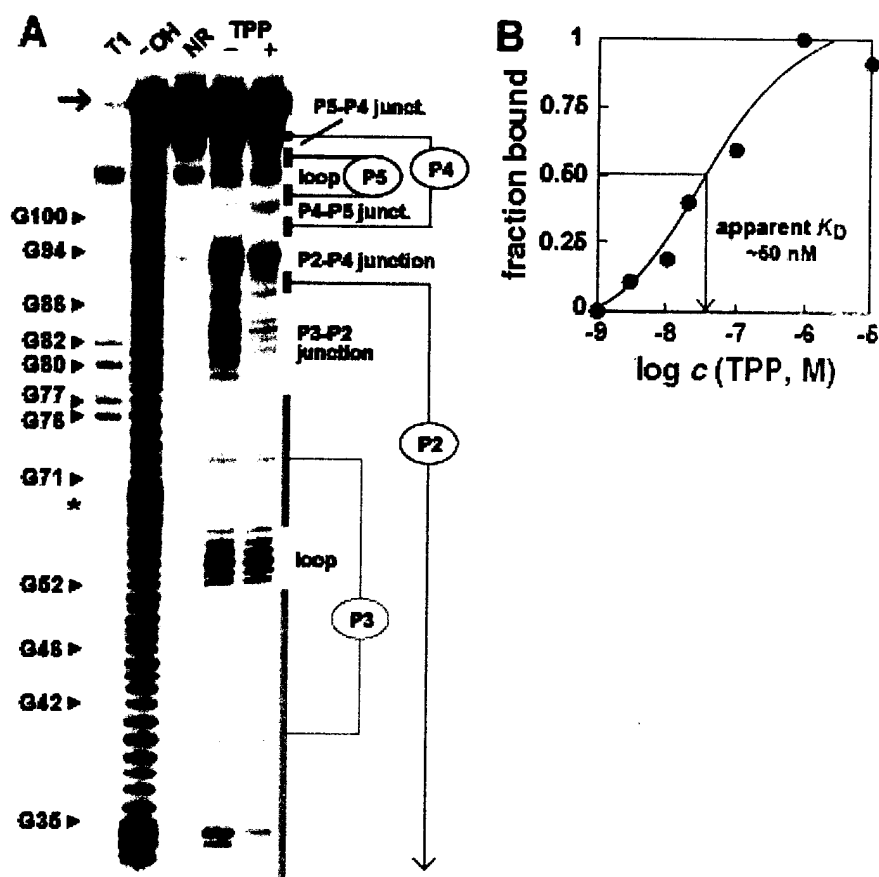


FIG 16

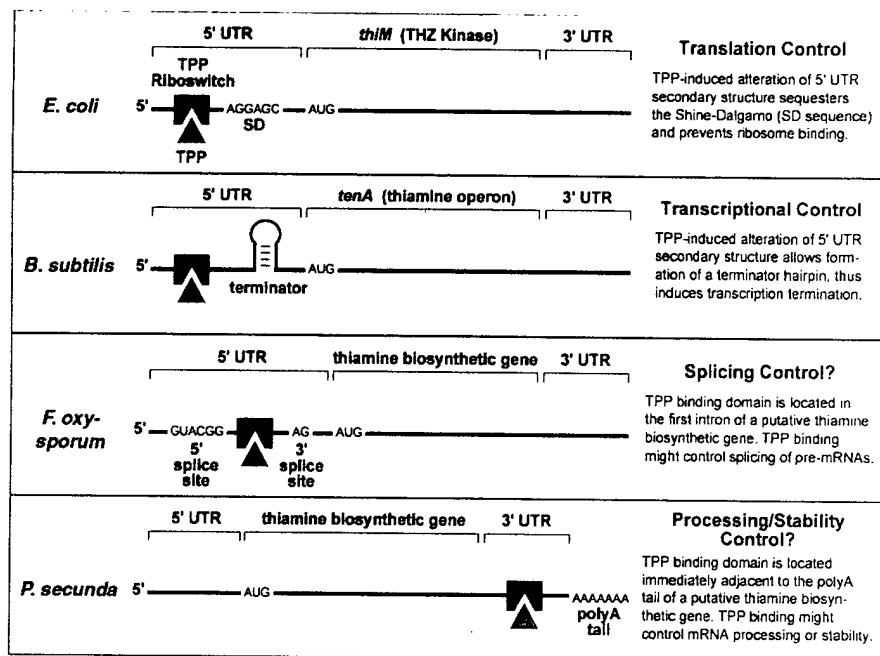


FIG 17

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1 BA 0845 CGGUGAAGU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUG- AU GAUGA AGGAUUA G-AAA AUAUAU
 2 BA *lysA* CUCAUAGGU AGGCC GAUA AG AAGAGUA AATTAAT G-AG- AAGUG- AU GAUGA AGGAUUA G-AAA AUAUAU
 3 BA *lysP* CGAAGAGGU AGGUU GAUUAU AAG-AGUA AATTAAT G-AGAU GAGAA- AU GAUGA AGGAUUA G-AAA AUAUAU
 4 BH *dapA* AGUGAAGAU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 5 BH *lysC* AGUGAAGGU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 6 BH *nhc* AGUGAAGGU AGGA- AATTAAT AAG-AGUA AATTAAT G-AGGUA GAGAA- AAGGCG- CGAAG-AAAA- CUC
 7 BS *lysC* CGUGAAGGU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 8 CA *lysA* AGUGAAGGU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 9 CP *lysA* GAGCAAAAU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 10 CP *lysP* AACUGAAGU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 11 CP *nhc* AAAAAAGU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 12 EC *lysC* CAGGCGAGA AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 13 HI *nhc* UACAAAGU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 14 OT *dapA* GUUUUGAU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 15 OT *nhc* UCGGUGGU AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 16 PM *nhc* UACUGUAGU AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 17 BA *lysC* AUAUAUAU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 18 SA *lysP* AUAUAUAU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 19 SE *lysC* AGAUUUAGU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 20 SE *lysP* AUAUAUAU AGGUU AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 21 SF *lysC* CAGGCGAGA AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 22 SO *lysC* AGGAGAGA AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 23 SO *nhc* GUUUUAUAU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 24 TH *aad* UAGGCGGAGU AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 25 TT *lysA* AGGAGAGA AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 26 TT *popF* CAGUAUAU AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 27 VC *lysC* UCUAGAGA AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 28 VC *nhc* UCUAGAGA AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 29 VC *lysC* UCUAGAGA AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 30 VV *lysC* UCUAGAGA AGGA- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU
 31 VV *nhc* UCUAGAGA AGGC- AATTAAT AAG-AGUA AATTAAT G-AG- AAGUGAGA CGGUGAGAUAUUG G-AAA AGAA- UUU

1 P3 CCACCAU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 2 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 3 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 4 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 5 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 6 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 7 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 8 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 9 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 10 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 11 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 12 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 13 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 14 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 15 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 16 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 17 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 18 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 19 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 20 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 21 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 22 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 23 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 24 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 25 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 26 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 27 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 28 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 29 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 30 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG
 31 P3 CCACU- P3' P4 CUGGUGAUAUA- P4' P5 CCGACAAAGGUU- P5' P1' AUGGAGAGG

FIG 18

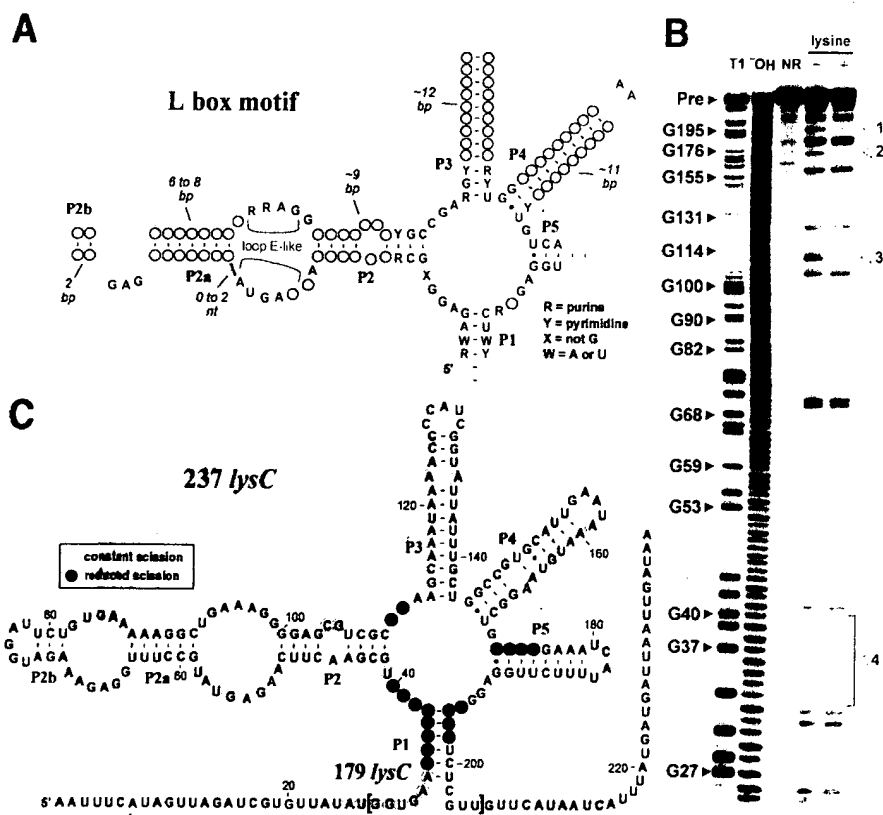
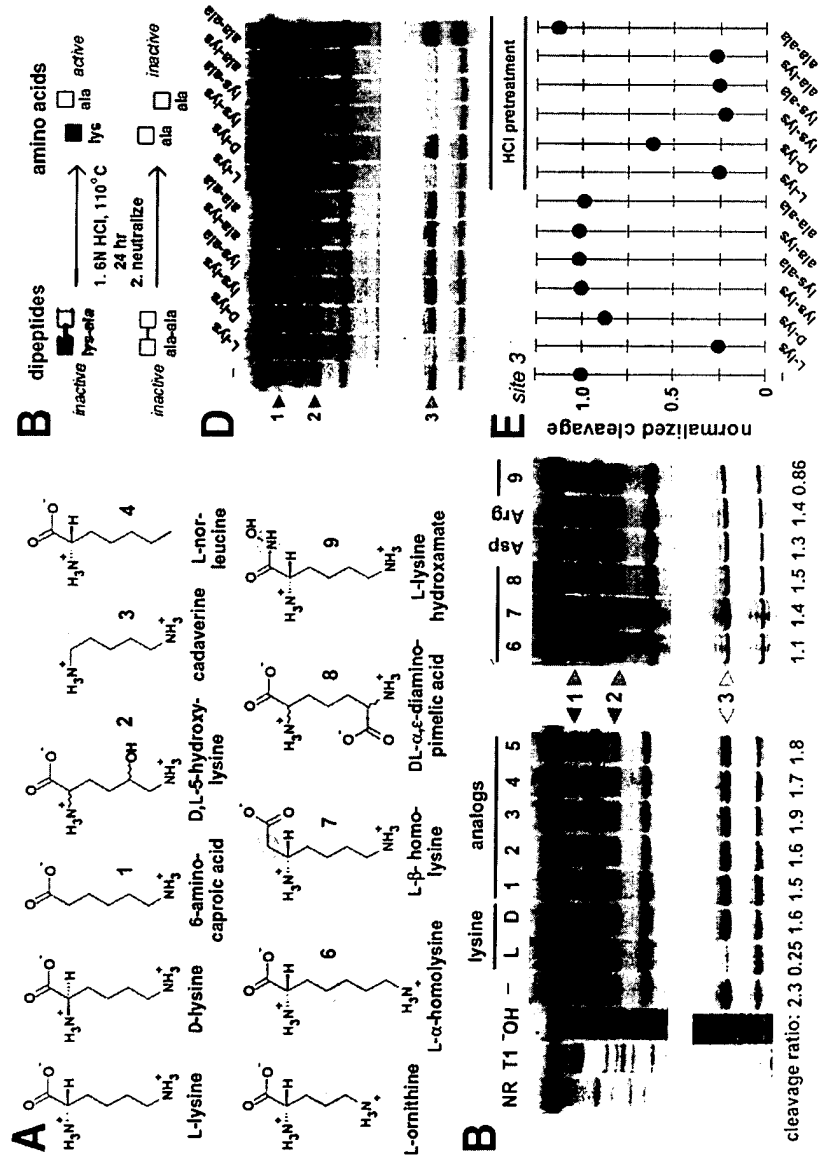


FIG. 19



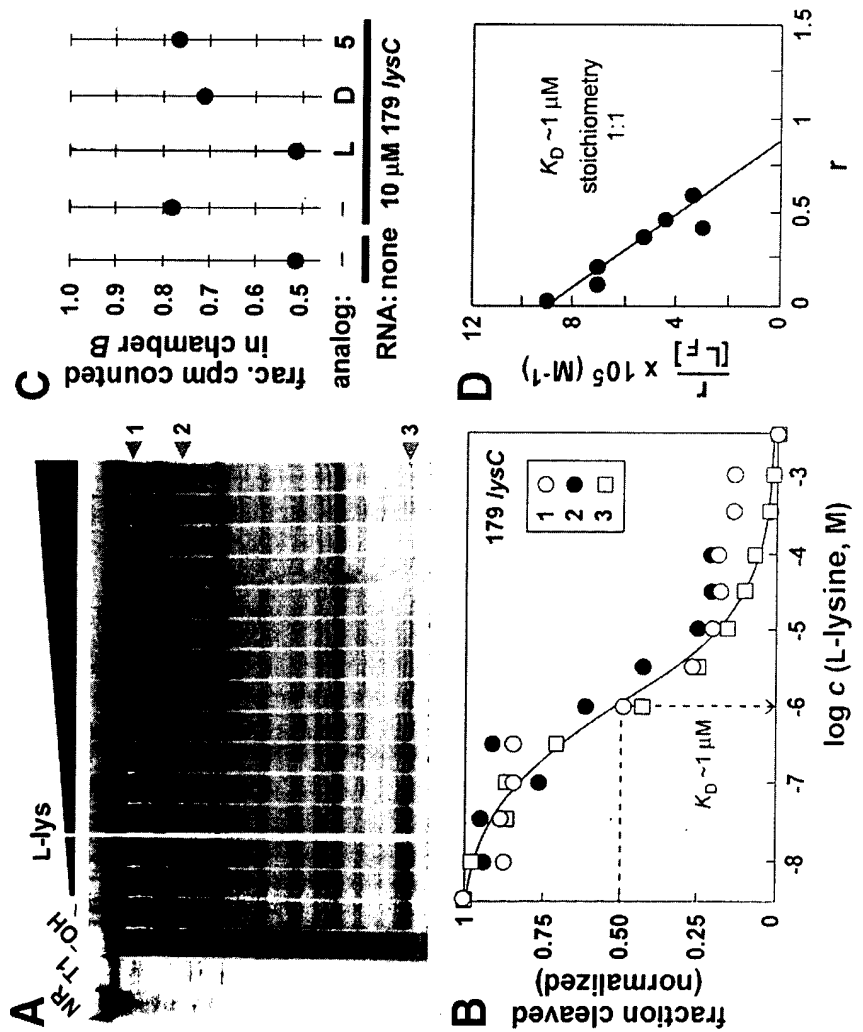


FIG 21

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[illegible]

FIG 23

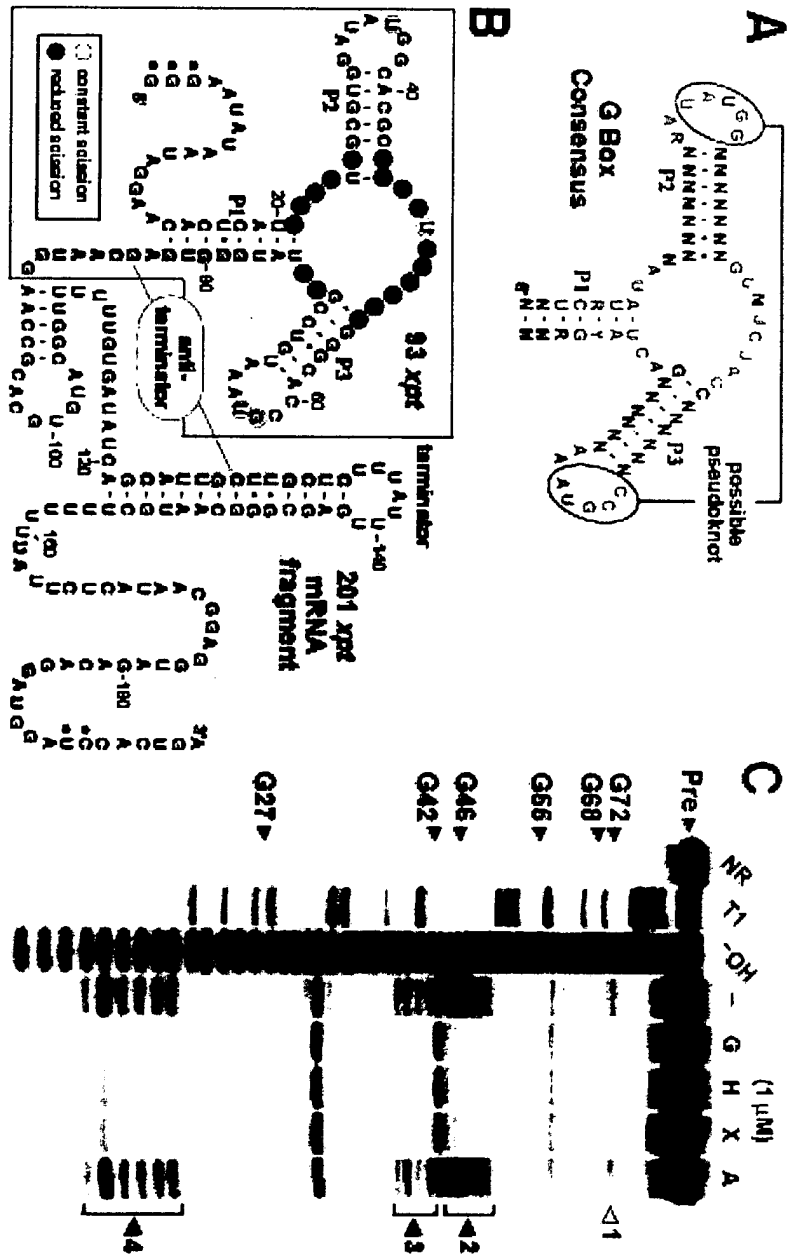


FIG 24

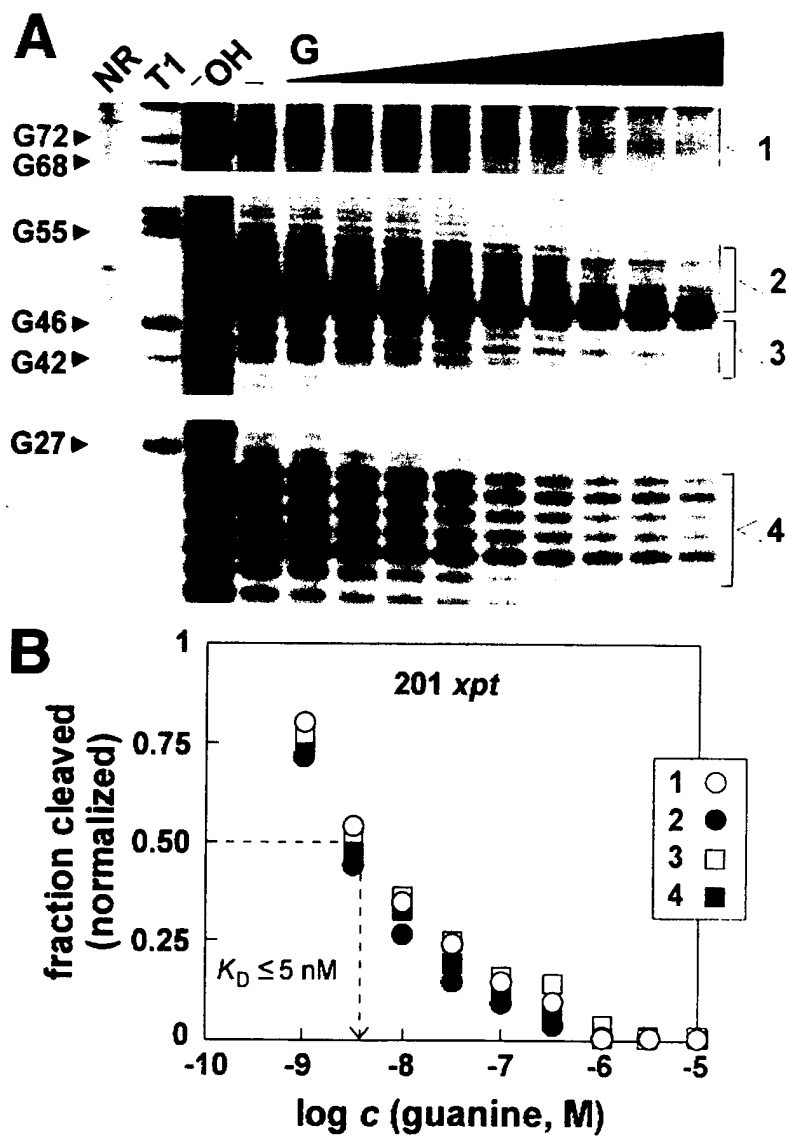


FIG. 25

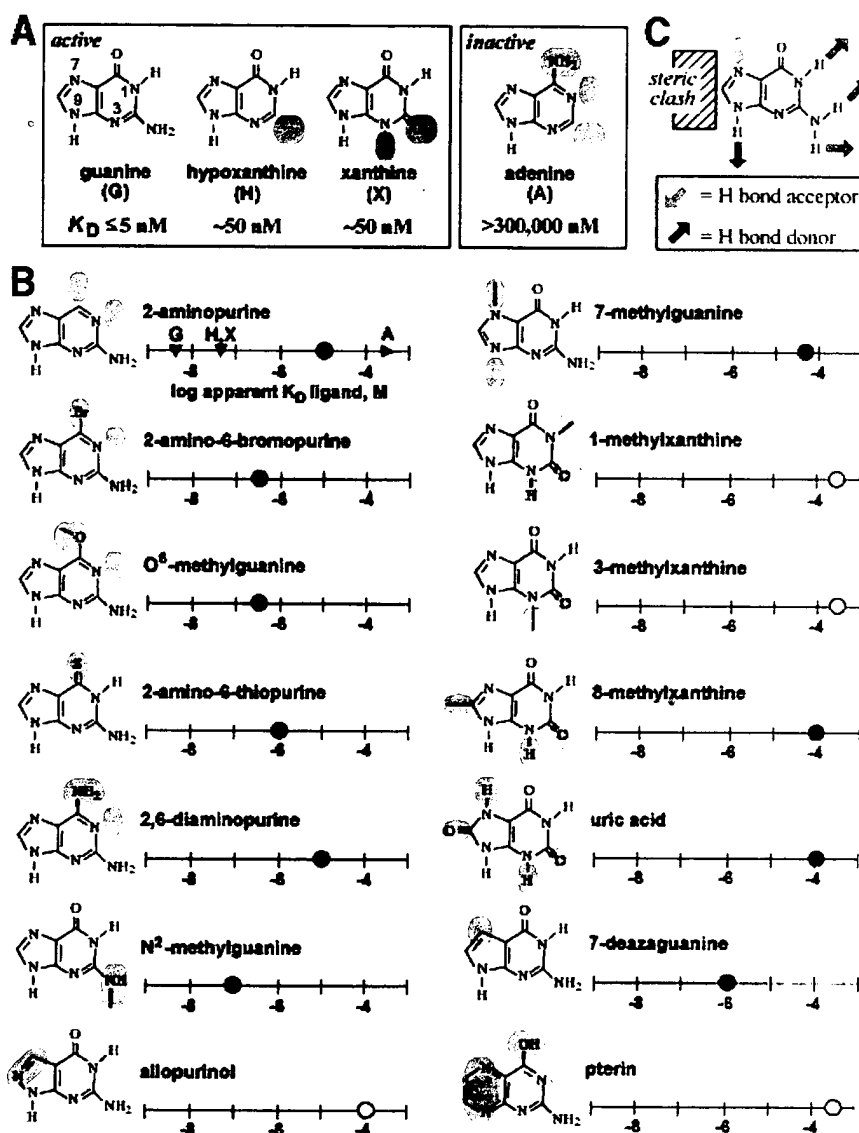


FIG 26

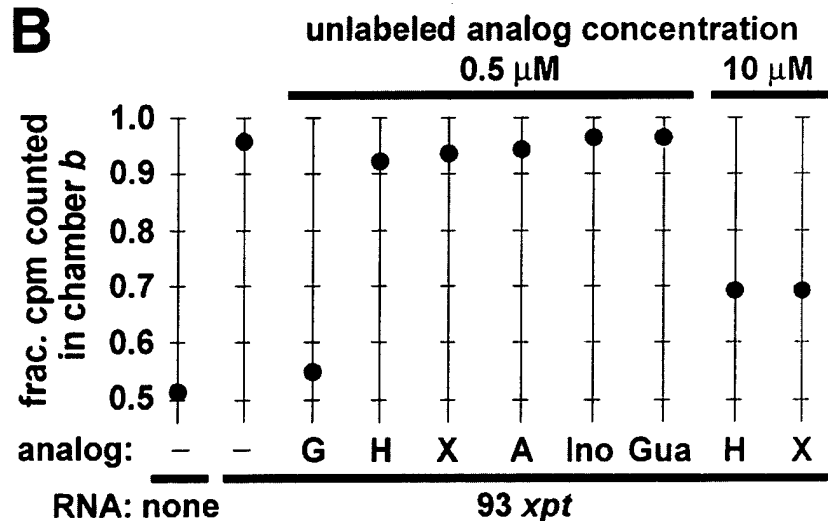
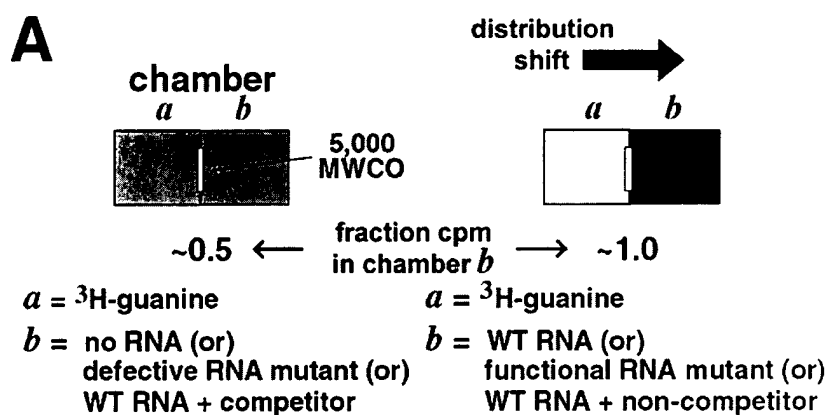


FIG 27

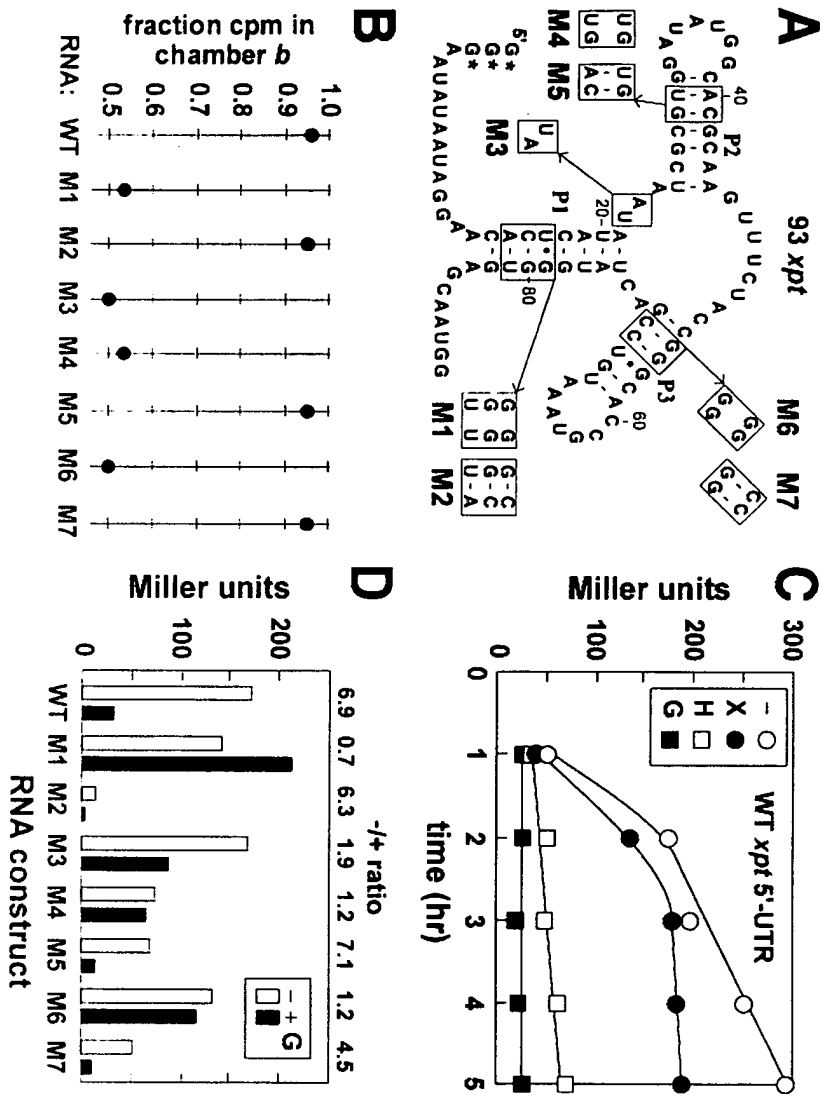


FIG. 28

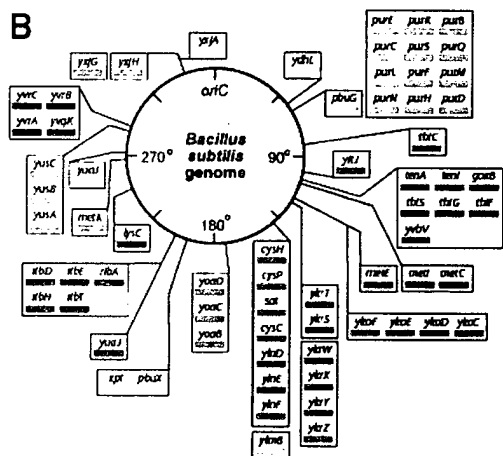
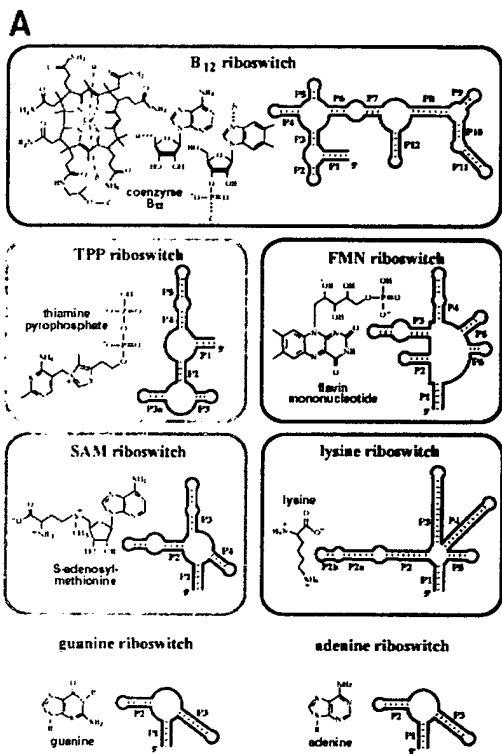


FIG. 29



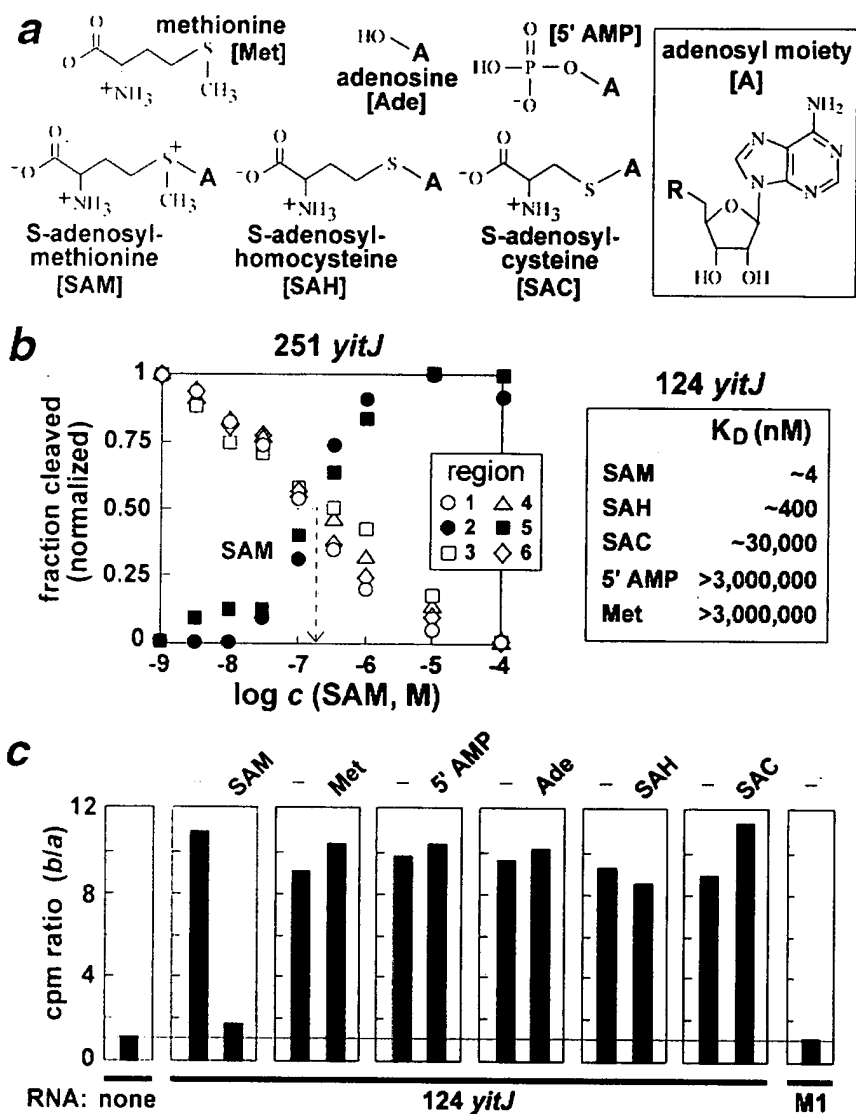


FIG. 31

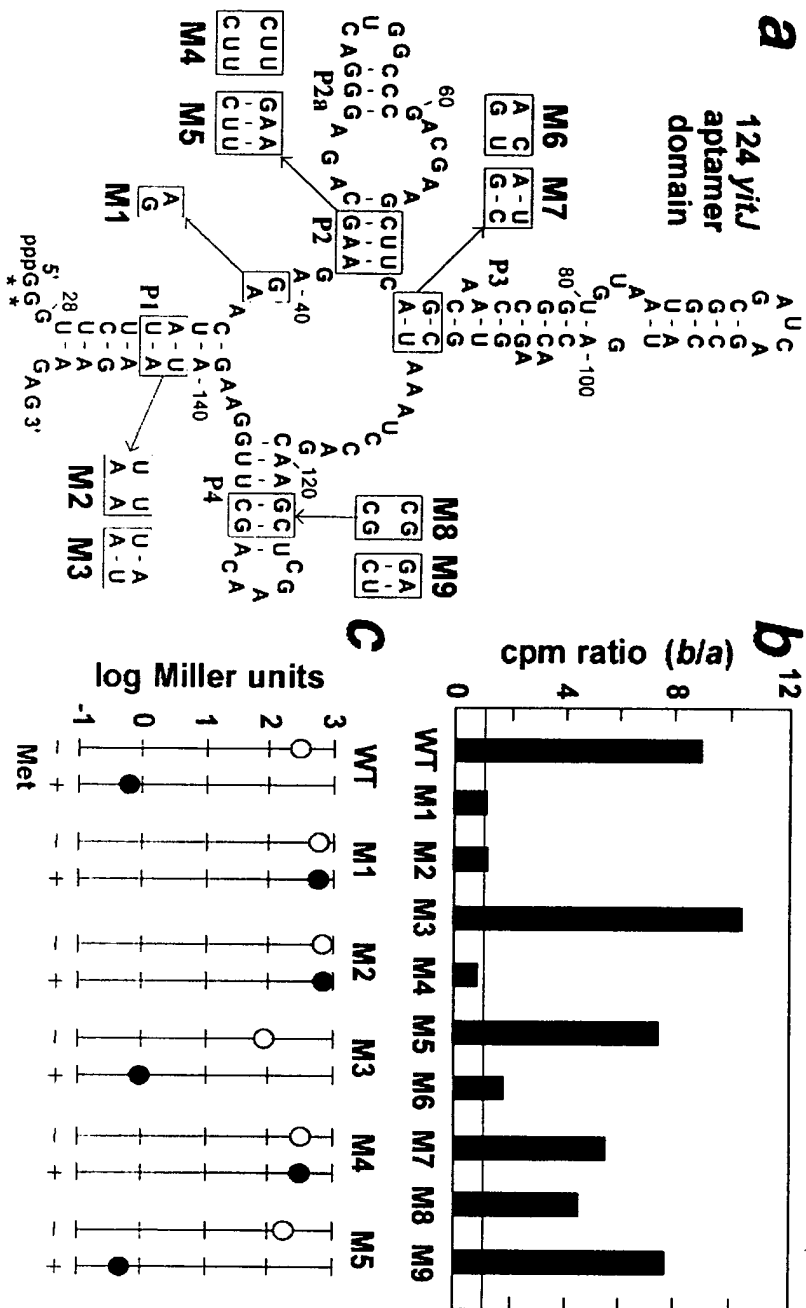


FIG. 32



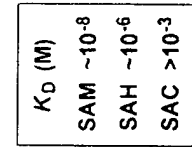


FIG. 34

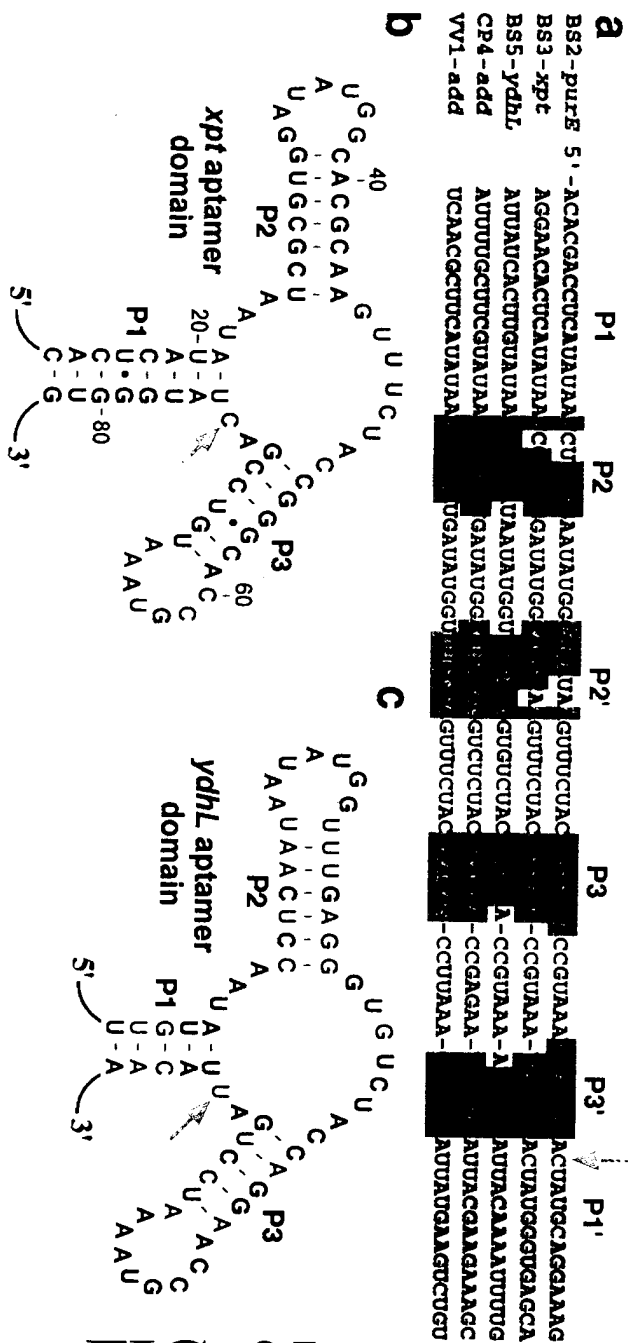


FIG. 35

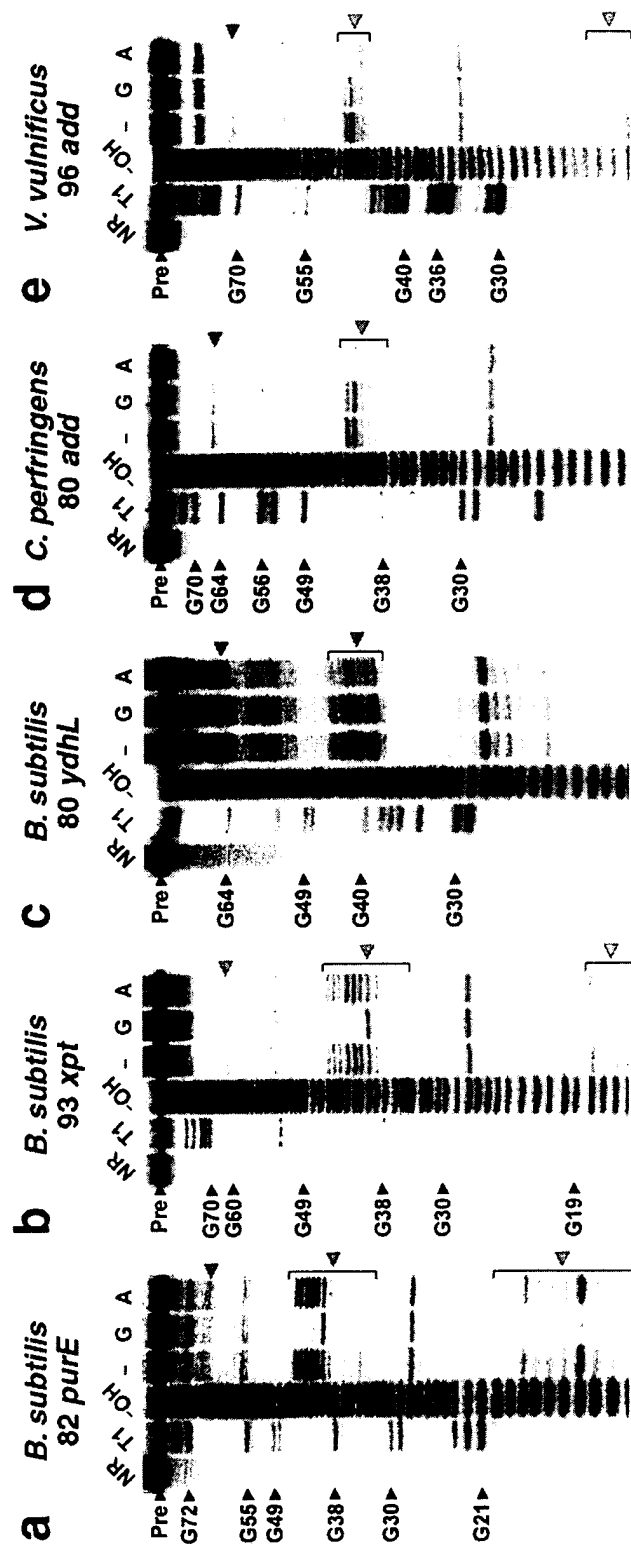


FIG 36

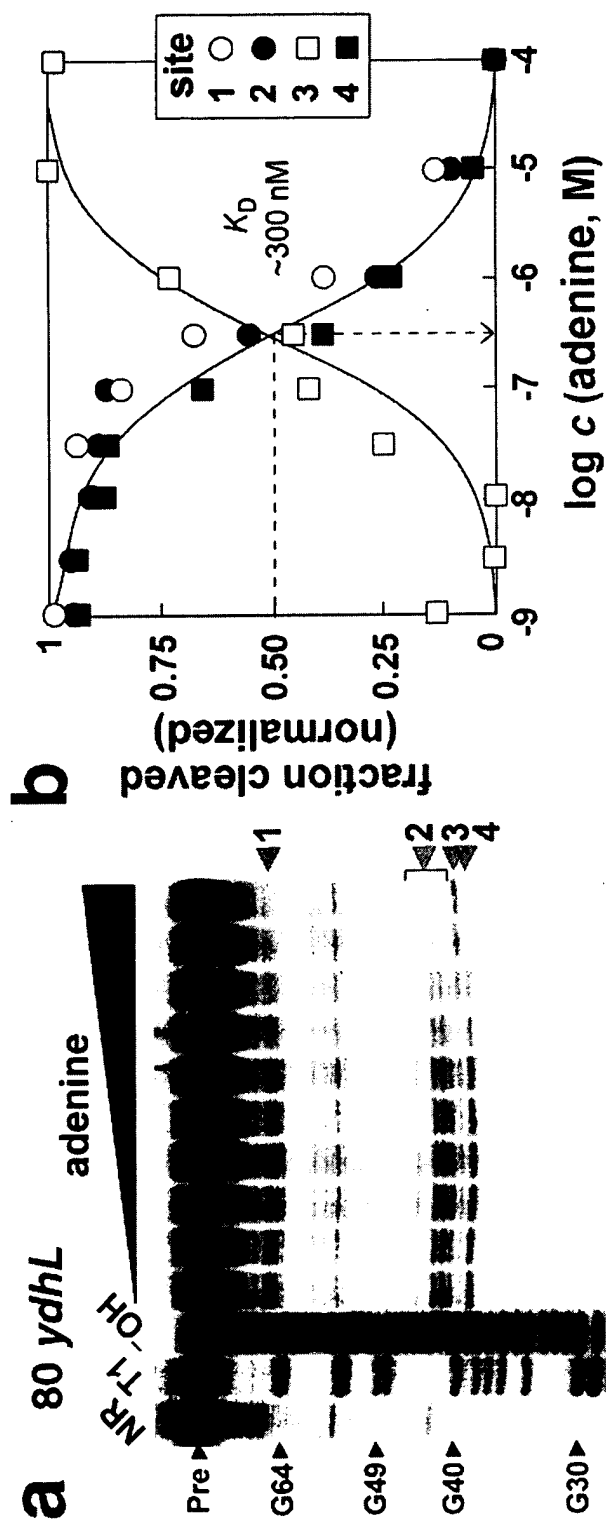


FIG 37

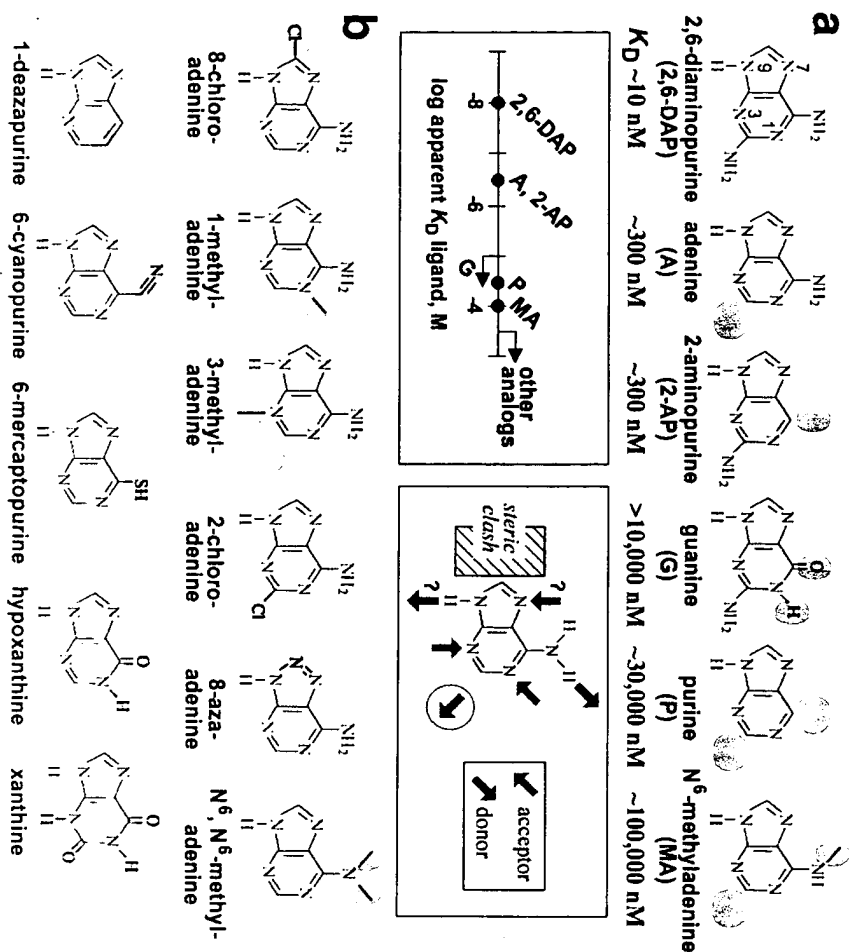


FIG. 38

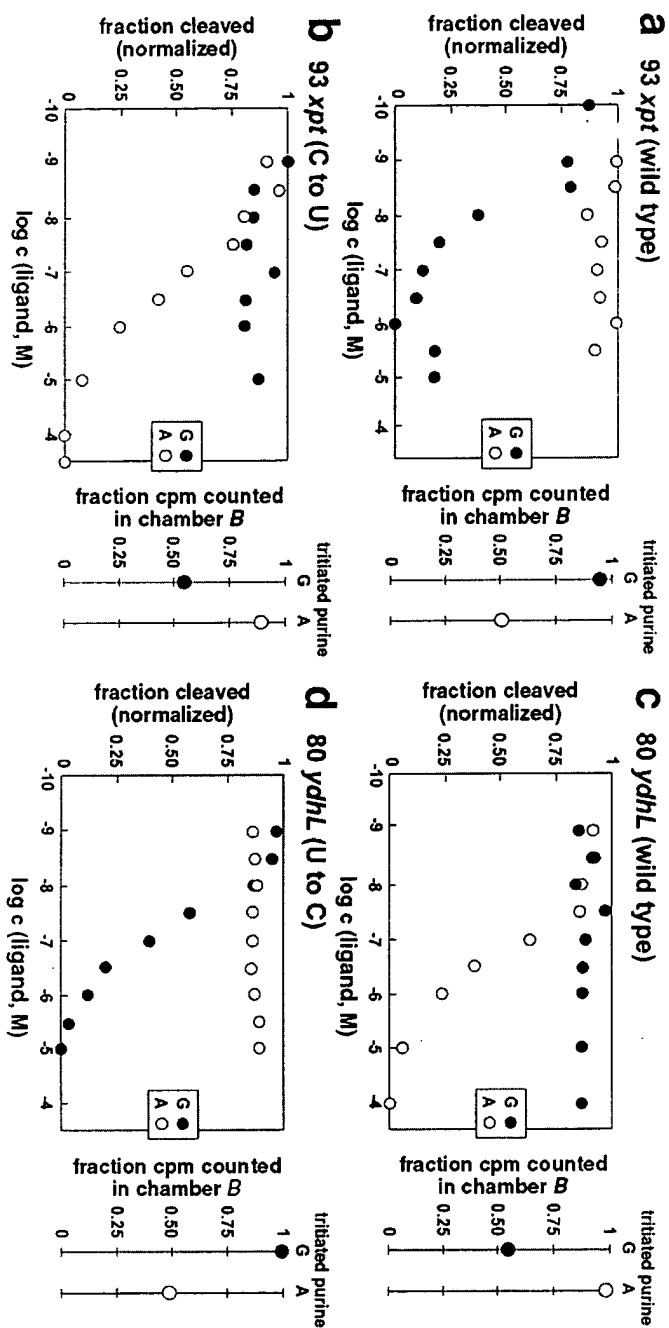


FIG. 39

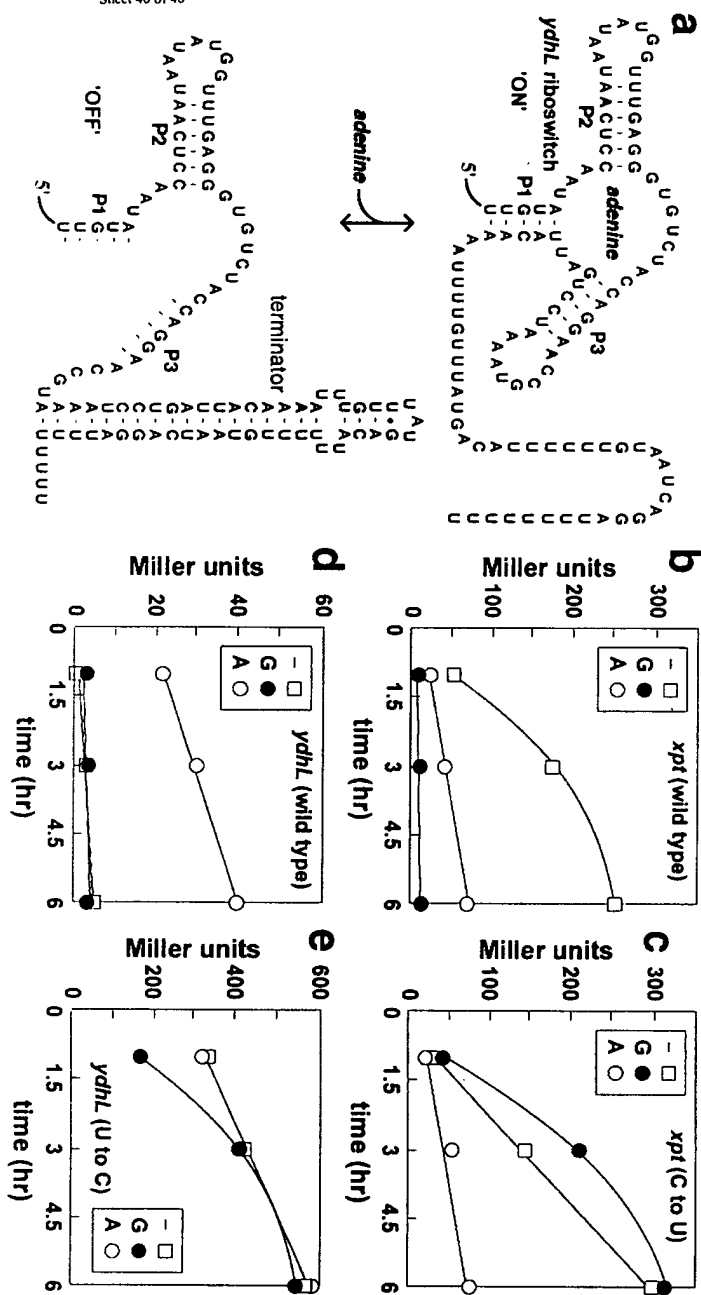


FIG. 40

Figure 41

A. Alignment of SAM Riboswitches.

Table S1. S Box Sequence Alignment					
ID	Position	Genbank Acc.	Organism	Remark	Start Operon
Bs01	- 1180274	NC_000964.1	Bacillus subtilis		92 metF (yitI)
Bs02	+ 1257777	NC_000964.1	Bacillus subtilis		70 metB-metC (yjcI)
Bs03	- 1385353	NC_000964.1	Bacillus subtilis		130 metE (metC)
Bs04	- 1424147	NC_000964.1	Bacillus subtilis	(*)	89 ykrT-GCN3 (ykrT)
Bs05	+ 1426344	NC_000964.1	Bacillus subtilis		60 rbcL-ykrX-araD-ykrZ (ykrW)
Bs06	+ 1629516	NC_000964.1	Bacillus subtilis		164 cysH-pitA-MET3-cysC (cysH)
Bs07	- 2024504	NC_000964.1	Bacillus subtilis		86 ldhA-xylB (yodD)
Bs08	- 3128412	NC_000964.1	Bacillus subtilis		170 metK (metE)
Bs09	- 3363560	NC_000964.1	Bacillus subtilis		108 abc -2011-nlpA (yusC)
Bs10	+ 3996569	NC_000964.1	Bacillus subtilis		85 metE (yxjH)
Bs11	+ 3997959	NC_000964.1	Bacillus subtilis		80 metE (yxjG)
Bh01	- 910190	NC_002570.1	Bacillus halodurans		141 ????
Bh02	+ 1348818	NC_002570.1	Bacillus halodurans		99 thrA
Bh03	+ 1699959	NC_002570.1	Bacillus halodurans		175 metB-metC-metF-metH

Bh04 - 3427466 NC_002570.1	Bacillus halodurans	157 metK
Bh05 - 3591166 NC_002570.1	Bacillus halodurans	220 abc-2011-nlpA
Oi01 + 727028 NC_004193.1	Oceanobacillus iheyensis	78 metH
Oi02 - 1098097 NC_004193.1	Oceanobacillus iheyensis	162 metE
Oi03 + 1319043 NC_004193.1	Oceanobacillus iheyensis	76 ????
Oi04 - 2134364 NC_004193.1	Oceanobacillus iheyensis	56 abc-????-nlpA
Oi05 - 2365511 NC_004193.1	Oceanobacillus iheyensis	176 metK
Oi06 - 2437305 NC_004193.1	Oceanobacillus iheyensis	129 abc-????-nlpA
Oi07 - 2708643 NC_004193.1	Oceanobacillus iheyensis	177 tran-MET17
Oi10 - 3200636 NC_004193.1	Oceanobacillus iheyensis	81 ????-????
Oi08 - 2856863 NC_004193.1	Oceanobacillus iheyensis	201 ????-????
Oi09 + 3162075 NC_004193.1	Oceanobacillus iheyensis	105 MET17
Oi10 - 3200636 NC_004193.1	Oceanobacillus iheyensis	81 ????-????
Oi11 + 3200766 NC_004193.1	Oceanobacillus iheyensis	94 ????
Oi12 + 3294474 NC_004193.1	Oceanobacillus iheyensis	97 abc-2011-nlpA-abgB
Oi13 - 3466518 NC_004193.1	Oceanobacillus iheyensis	112 gldA-nlpA-abc-2011
Ca01 + 453565 NC_003030.1	Clostridium acetobutylicum	78 metB-metC
Ca02 - 671354 NC_003030.1	Clostridium acetobutylicum	77 metH
Ca03 - 1073886 NC_003030.1	Clostridium acetobutylicum	(smtA-metB-cysK)
Ca04 + 1131539 NC_003030.1	Clostridium acetobutylicum	81 abc-2011-nlpA

(1)

(2)

Ca05 + 1976373 NC_003030.1	Clostridium acetobutylicum	102	metA
Ca06 - 2914839 NC_003030.1	Clostridium acetobutylicum	117	CAC5
Ca07 - 2991405 NC_003030.1	Clostridium acetobutylicum	70	metK
Cp01 - 2500081 NC_003366.1	Clostridium perfringens	391	metK
Cp02 - 2665229 NC_003366.1	Clostridium perfringens	102	nhaC
Lm01 + 137135 NC_003210.1	Listeria monocytogenes	90	oppA-dppB-dppC
Lm02 - 309383 NC_003210.1	Listeria monocytogenes	113	nlpA-abc-2011
Lm03 - 637924 NC_003210.1	Listeria monocytogenes	111	MET17-MET2
Lm04 + 882772 NC_003210.1	Listeria monocytogenes	97	metE
Lm05 - 1716649 NC_003210.1	Listeria monocytogenes	110	metK
Lm06 - 1739595 NC_003210.1	Listeria monocytogenes	109	metE-metB-metC-metH
Lm07 - 2491174 NC_003210.1	Listeria monocytogenes	93	abc-2011-nlpA
Li01 + 172401 NC_003212.1	Listeria innocua	88	oppA-dppB-dppC
Li02 - 327333 NC_003212.1	Listeria innocua	113	nlpA-abc-2011
Li03 - 636911 NC_003212.1	Listeria innocua	111	met17-met2
Li04 + 871751 NC_003212.1	Listeria innocua	97	metE
Li05 - 1772459 NC_003212.1	Listeria innocua	110	metK
Li06 - 1790189 NC_003212.1	Listeria innocua	109	metE-metB-metC-metH
Li07 - 2538251 NC_003212.1	Listeria innocua	92	abc-2011-nlpA
Sa01 + 15958 NC_002745.1	Staphylococcus aureus	41	met2

Sa02 + 875385 NC_002745.1	Staphylococcus aureus	91 abc-2011-nlpA
Sa03 - 1844603 NC_002745.1	Staphylococcus aureus	108 metK
Sa04 - 2381620 NC_002745.1	Staphylococcus aureus	13 nhaC
Sc01 + 4708438 NC_003888.1	Streptomyces coelicolor	26 thrC-moaD

ID	Position	Genbank Acc.	Organism	Remark	Start Operon
Ct01	+	606192	AE_006470	Chlorobium tepidum	107 CAC5-MET2
Tt01	+	500245	NC_003869.1	Thermoanaerobacter tengcongensis	55 metK
Tt02	-	1750367	NC_003869.1	Thermoanaerobacter tengcongensis	66 metF-metH-ebsC
Tt03	-	2076680	NC_003869.1	Thermoanaerobacter tengcongensis	78 thrA-CAC5
Fn01	-	987483	NC_003454.1	Fusobacterium nucleatum	84 metK
Fn02	-	1317650	NC_003454.1	Fusobacterium nucleatum	91 abc-2011-nlpA
Dr01	+	1363063	NC_001263.1	Deinococcus radiodurans, chr 1	156 abc-2011-nlpA-nlpA
Dr02	+	980704	NC_001263.1	Deinococcus radiodurans, chr 1	41 metH-???-metF
Xa01	-	3558018	NC_003919.1	Xanthomonas axonopodis	74 MET2-metC-thrA
Xc01	-	3379769	NC_003902.1	Xanthomonas campestris	73 MET2-metC-thrA
Se01	+	574	AF_269983.1	Staphylococcus epidermidis genomic clone	
Se02	-	142	AF_270301.1	Staphylococcus epidermidis genomic clone	(*)
Gs01	+	342843	contig:2947	Geobacter sulfurreducens	
Gs02	+	2470946	contig:2947	Geobacter sulfurreducens	
Ba01	-	177272	contig:6615	Bacillus anthracis	
Ba02	+	185586	contig:6615	Bacillus anthracis	
Ba03	-	197185	contig:6615	Bacillus anthracis	
Ba04	+	320607	contig:6615	Bacillus anthracis	

Ba05 - 371127	contig:6615	Bacillus anthracis	
Ba06 + 1362659	contig:6615	Bacillus anthracis	
Ba07 + 1375353	contig:6615	Bacillus anthracis	
Ba08 + 2459362	contig:6615	Bacillus anthracis	
Ba09 - 2953226	contig:6615	Bacillus anthracis	
Ba10 - 3091676	contig:6615	Bacillus anthracis	
Ba11 - 3890736	contig:6615	Bacillus anthracis	
Ba12 + 3892933	contig:6615	Bacillus anthracis	
Ba13 + 4074285	contig:6615	Bacillus anthracis	
Ba14 - 4074078	contig:6615	Bacillus anthracis	
Ba15 - 4553682	contig:6615	Bacillus anthracis	(*)
Ba16 - 4739975	contig:6615	Bacillus anthracis	
Ba17 - 5140322	contig:6615	Bacillus anthracis	(*)
Bc01 + 26115	contig:1617	Bacillus cereus	
Bc02 + 748841	contig:1617	Bacillus cereus	(*)
Bc03 + 1183078	contig:1617	Bacillus cereus	(*)
Bc04 + 1195849	contig:1617	Bacillus cereus	(*)
Bc05 + 2200884	contig:1617	Bacillus cereus	(*)
Bc06 - 2684484	contig:1617	Bacillus cereus	(*)
Bc07 - 2963724	contig:1617	Bacillus cereus	

Bc08 - 2773209	contig:1617	Bacillus cereus	(*)
Bc09 + 3500608	contig:1617	Bacillus cereus	(*)
Bc10 - 3687209	contig:1617	Bacillus cereus	(*)
Bc11 + 3687417	contig:1617	Bacillus cereus	(*)
Bc12 - 3498410	contig:1617	Bacillus cereus	(*)
Bc13 - 4205859	contig:1617	Bacillus cereus	(*)
Bc14 - 4397125	contig:1617	Bacillus cereus	(*)
Bc15 - 4784934	contig:1617	Bacillus cereus	(*)
Bc16 - 5114094	contig:1617	Bacillus cereus	(*)
Bc17 - 5094322	contig:1617	Bacillus cereus	(*)
Bc18 + 5101784	contig:1617	Bacillus cereus	(*)

Bs01 ATATCCGTTCTTATC AAGAGC AAGCAGAGGGGA CTGG CCCGACGAAAGCTT CAGCA CCGGTGTAA TGGC GATCA
 Bs02 TCGATA TTCTTATCTGTAGC AGGTGAGGGGA CTGG CCC TTAGA ACCCT CAGCA CCGGCTTGT TTTGC ATTT
 Bs03 ACA TTCTCTCTATC GAGAGC TTGGGCGA GGGGA TTGG CCC TTGAC CCCCA CAGCA CCGACC GTAATC CATTGTGAAATGG GGGGCACTGCTTTTTC GCGCCGAGAGC
 Bs04 ATATA TTCTCTATC GAGAGC TTGGGCGAGGGAT TTGG CCC TTGAC CCCCA AAGCA CCGACC GTAATCCATTGTGAAATGG GGGGCA TTTTTTTC GCGCCGAGAGC
 Bs05 CTATATTTCTTATC AAGAACA GGGAGAGGGGA CTGG CCC GATCAAGCC GGGCA CCGACTT ATA
 Bs06 ATCTAAAACTTATCAAGAGC GGTGAGGGGA CTGG CTTATGAAGCC GGGCA CCGTGA TAGTT
 Bs07 TCAATA TTCTTATCTCAGAGC AGGTGGAGGGGA CTGG CCC TATGAAGCTT GGCACA TTAT
 Bs08 GCGGAA TACTTATCTCCGAGCT GGGGAGAGGGGA CAGG CCC TATGAAGCC CAGCA CCGGTTTCTC TGTTATTATTA TGTCAACTGAGT
 Bs09 TATA TTCTCTCTATCAAGACA GGTGGAGGGGA ATGG CCC TATGAAGCC GGGCA CCGATCAAC ACT
 Bs10 AAGTTGTA CTTATCTAAGAGA GGTGGAGGGGA CTGG CCC ATGATACC GGGCA CCGCTGTT TCA
 Bs11 AAGGTTTTCTTATCAAGACA GGTGGAGGGGA CTGG CCC TCGCATACC GGGCA CCGCTGT TTA
 Bh01 TCATA TTCTTATCTCAGAGT GGTGGAGGGGA CTGG CCC TGTGAAGCC GGGCA CCGCTTT TTTT
 Bh02 ATAAAAAGACTTATCTGAGAGA GGGAGAGGGGA CTGA CCCGATGATGCC GGGCA CCGGTTTGT AGCCA
 Bh03 TCTCGTATTTCTTATCTCAGAGC AGGTGGAGGGGA CAGG CCCGAGAGAAAGCT CAGCAACCAAGCCATC ATCC
 Bh04 ACGGATATCTTATCTCAGAGT GGTGGAGGGGA CTGG CCCGATGAAAGCC CAGCAACCGCCAAAGC AGCAATC
 Oi01 ATAGTTAGAACTTATCTAAGAGC AGATGAGGGGA TTGG CCCGATGAAGTCT CAGCA CCGAGCT AGATA
 Oi02 ATGACAA TTCTTATCTCAGAGC AGGTGAGGGGA CTGG CCCAAGCAAGCTT GGGCA CAGACTTA TTGAT
 Oi03 ATGAAAA TCTTATCTAAGAGC AGGTGGAGGGGA CTGG CCCGCTGAAAGCTT CAGCAACAGA ACGCATCTG
 Oi04 ATTGAATAA CTTATCTCAGAGC TGACGAGGGGA CAGGA CTTA CCA TGTCA CAGCA CCGTACC TTAC
 Oi05 ACGGATATCTTATCTCAGAGT GGTGGAGGGGA CAGA CCCGATGAAAGCC CAGCAACCAATCACT ACT
 Oi06 ATGATA TCTTATCTTAGAG CCGTGGAGGGGA CTGG CCC TTGAAAGCC GGGCA CCGTTGAT AATTAA
 Oi07 TACGTTTTCTTATCTAGAT AGGCGAGGGGA ATGG CCC AACGAAGCT GGGCA CAGGTTCT TATT
 Oi10 ATGAAATA TCTTATCTAGAG AGGTGAGGGGA ATGG CCC AAAAGAGCTT GGGCA CAGGTTG TAGCTT
 Oi08 TTATTTTCTTATCTAAGAGT CCGGCGAGGAAT CTGG CCC ATGATCCCG CAGCA CCGTTAG AATGA
 Oi09 AGCAAA TCTTATCTAAGAGT GGTGGAGGGGA ATGG CCC TCGGAAGCC GGGCA CCGTATGG AATT
 Oi10 ATGAAATA TCTTATCTAGAG AGGTGAGGGGA ATGG CCC AAAAGAGCTT GGGCA CAGGTTG TAGCTT
 Oi11 TTAATACTTCTTATCTGAGAG AAGCTAAAGGAC CTGG CTTTGACGCTT CAGCAAGCTTA TCTCCAT

Ohl2 AC GTTTT **TTTCTATG** TAGAG **AGAT** TGAGGGGAT **CAGG** **CCC** TATGAC **ATGT** **GGCA** CGGATTCCTTA **TAT** **TAT** **TTT**
Ohl3 CTAATA **CTCTTATG** GAGAGT **GGC** TGA **GGGA** **GTGG** **CCC** TGTGAC **GGC** **GGCA** ACGGTTCATCGT **AATTCCA**
Ca01 TAA TTGT **TTCTTATC** AAGA GT **CAC** GGAGGGA **TAGG** **CCC** TATGA **GTG** **GGCA** CATCCAA **TTATT**
Ca02 TGTAAAA **CTTATC** AAGA GT **GGT** GAGGGA **GTGG** **CCC** TTTGA **ACC** **GGCA** ACCAGTATAT **TTTT**
Ca03 TAATA **TTCTTATC** AAGA **AAAG** GGA **GGGA** **GTGG** **CCC** AATGAT **GTGT** **CAGCA** ACCAAGT **TTTAT**
Ca04 ATTAGTCA **TTTATC** AAGA GA **GGT** GAGGGA **GTGG** **CCC** TGTGA **GGC** **CAGCA** CCGTGTATA **TGTTAAT**
Ca05 ATATTA **TTTCTATC** AAGA **GGT** GGA **GGGA** **GTGG** **CCC** TATGAA **GGC** **TGACA** ACGGGC **AAAT**
Ca06 TGA TAAGG **TTTATC** AAGA GA **GGT** GAGGGA **GTGG** **CCC** TATGA **ACC** **CAACA** CCAGCATTT **TTTAATT**
Ca07 ATGGAAA **CTCTTATC** AAGA GA **GGT** GAGGGA **ATGG** **CCC** GTTGA **ACC** **GGCA** CCGATGTAT **AATTTA**
Cp01 TTATATA **CTCTTATC** CAGA GA **GGT** GGA **GGG** AAAAA **GG** **CCC** TATGAA **ACC** **GGCA** ACGAGTGA **GAAA**
Cp02 TTAATAAA **CTTATC** AAGA GA **GGT** GGA **GGGA** **GTGG** **CCC** TGTGA **ACC** **CAGCA** ACGGTAA **TCCTTTGCGGTTAAAA** CAA **TCGTCGATTTTAAAA** TAAAA **AAAAATCAGTAGTA**
Lm01 TTACGTTT **CTTATC** AAGA GT **GGT** GGA **GGGA** **ATGG** **CCC** AGTGA **ACC** **CAGCA** CCGGAGC **GCAA**
Lm02 ATAT **TTTCTTATC** GAGA GC **GGC** AGA **GGGA** **GTGG** **CCC** GATGA **GGC** **GGCA** AACCTAACCTTTAT **TTAAGC**
Lm03 TAGTATTT **CTTATC** ACGAA **AGGT** GGA **GGGA** **GTGG** **CCC** TTTGAA **GGCT** **TAGCA** ACGGAA **TTTAT**
Lm04 ACATAGTAA **CTTATC** AAGA GA **AGGT** GAGGGT **TTGTGG** **CCC** CGTGA **GGCT** **TGGCA** CCGGA **TTTT**
Lm05 AATTAT **CTCTTATC** CAGA GC **GGT** AGA **GGGA** **GTGA** **CCC** TTTGAA **GGC** **CAGCA** ACGTACAG **ATATAA**
Lm06 TAAATTG **CTCTTATC** AATGAGT **GGT** AGA **GGGA** **GTGG** **CCC** GTTGA **ACC** **GGCA** ACGTTTCAA **TACG**
Lm07 TGTAGAAA **CTTATC** CAGA GT **GGT** GAGGGA **ATTC** **CCC** TATGA **GGC** **CAGCA** ACGTAAACAATAA **TTCA**
Li01 TTACAAATT **CTTATC** CAGA GT **GGT** GGA **GGG** AA **TTGG** **CCC** AGTGA **ACC** **GGCA** CCGGAGC **GCAA**
Li02 ATAT **TTTCTTATC** GAGA GC **GGC** AGA **GGGA** **GTGG** **CCC** GATGA **GGC** **GGCA** ACGTAACTTTAT **TTAAGC**
Li03 TAGTATTT **CTTATC** ACGAA **AGGT** GGA **GGGA** **GTGG** **CCC** TTTGAA **GGCT** **TAGCA** ACGGAA **TTTAT**
Li04 ACATAGTAA **CTTATC** AAGA **AGGT** GAGGGT **TTGTGG** **CCC** AGTGA **GGCT** **TGGCA** CCGGA **CTTT**
Li05 AATTTAT **CTCTTATC** CAGA GC **GGT** AGA **GGGA** **GTGA** **CCC** TTTGAA **GGC** **CAGCA** ACGTAGAC **ATATAA**
Li06 TAAATTAT **CTCTTATC** ATGAGT **GGT** AGA **GGGA** **GTGG** **CCC** GTTGA **ACC** **CAGCA** ACGTTTCAA **TTCG**
Li07 TGTAGAAA **CTTATC** CAGA GT **GGT** GAGGGA **ATTC** **CCC** TGTGA **ACC** **CAGCA** ACGTAAACAATAA **TTCA**
Sa01 TTCATATTT **CTTATC** GTGAG **AGGT** TGA **GGG** AC **TTGG** **CCC** TGTGAT **AGCT** **CAGCA** CCGACT **TTAT**
Sa02 GCGTAAA **CTCTTATC** GAGA GT **GGT** GAGGGA **TTTG** **CCC** TACGA **GGC** **GGCA** CCGTCTT **ATATA**
Sa03 ACGGATT **CTCTTATC** CTGAGT **GGT** GGA **GGG** AC **ATGG** **ACC** AATGA **ACC** **CAGCA** ACGTCTT **TTTAT**
Sa04 TAAGCATCA **CTTATC** TAGAG **AGGT** GGA **GGGA** **GTGG** **CCC** TATGA **GGCT** **GGGCA** AGAT **CTCGA**
Ss01 TTCATACCC **CTCATC** CAGA GC **GGC** AGA **GGG** AT **AGGG** **CCC** GATGA **AGCC** **GGGCA** CCGTGAAGTGG **TTCTTGTACACACGGACGTGGCGAGGCTC**

ConsycttATc.aGag--ggYrGAGGGA-y.gg---CCc..yGA Rec.-cRGAaC...y.....

C01 TTTGAGCTATCATCAGAA-AGGGGGAAGGA-CITGG-CCCTGCGAAAGCC-**TTGGCAACCTTCAT**-----TCCAC-----

T101 TAACACCGCTCTTATCAAGA-GA-**GGTGGAGGGA-AGAG-CCC**GATGA**ACC-GGGAACCTGTCT**-----TTAA-----

T102 TTAAATCTCTTATCAAGA-GA-**GGTGGAGGGA-CITGG-CCC**GATGA**ACC-GGGAACCTGTCT**-----TTAG-----

T103 CTCAA**TTCTCTTATC**AAAGAT-**GGTGGAGGA-CITGG-CCC**GATGA**ACC-GGGAACCTGTCT**-----GTAA-----

F01 TGGAAATAA**CCATCAAGAG-AGAT**TGA**GGGA-CAGG-CCC**GTTGAG**ATGT-CAGCAACCTAGG**-----TAAAA-----

F02 AAATAAATAA**CCATCAAGAG-AGAT**TGA**GGGA-CAGG-CCC**AAATGA**TGTT-CAGCAACCTAG**-----TTAAAT-----

D01 AGGTCA**CTTTATC**CAGAGT-**GGGCGCAAGGAC-CITGG-CCC**ATGAC**CCCG-CAGCAACCTGGC**-----CTCATCAC-----

D02 CCGTGC**CCGCTCATC**CAGAGT-**GGGCGCAAGGAC-CITGG-CCC**ATGAC**CCCG-CAGCAACCTGGC**-----TTCATCAC-----

Xa01 CCTAGCCTC**ACCATC**CAGAG-**GGGCGGAAGGA-CAGG-CCC**TTTGA**TGCGG-GGCAAGCCAAGGGAAGCG**-----GCAA-----

Xc01 CGTAGCCTC**ACCATC**CAGAG-**GGGCGGAAGGA-CAGG-CCC**TTTGA**TGCGG-GGCAAGCCAAGGGAAGCG**-----GCAA-----

Se01 TTACCTAAC**CTTAT**TTTGA-**AGGTGAAGGAT-TTGG-CCC**ATAGAA**GGT-CAGCAACCTGTCT**-----TTAAAT-----

Se02 ACGAT**CTTATC**CTAGT-**GGTGGAGGGAAC-ATGG-ACC**AAATGA**ACC-CAGCAACCTGTCT**-----ATT-----

Gs01 GTAGA**CTTCTTATC**AAAG-**TTGGTGGAGGGA-AGG-CCC**TCTGA**ACCA-CAGCAACCTGTCT**-----GTAG-----

Gs02 ACGGCTTA**CTTATC**AAAG-**TTGGTGGAGGGA-AGG-CCC**TCTGA**ACCA-CAGCAACCTGTCT**-----ATGG-----

Ba01 ACACATA**CTTCTTATC**AAAG-**TTGGTGGAGGGA-AGG-CCC**TCTGA**ACCA-CAGCAACCTGTCT**-----ACG-----

Ba02 AGCAAT**TTTATC**TTATCAGAG-**AGGTGGAAGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----GTAATA-----

Ba03 TTTA**CTCAT**TTGATCAAGAG-**AGGTGGAAGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----TTTT-----

Ba04 CGATACA**TTTCTTATC**CAGAG-**AGGTGGAAGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----TTTT-----

Ba05 GAATAAT**TTTCTTATC**AAAGAG-**GGCAGAGGGA-CITGG-CCC**TTTGA**AGCC-CAGCAACCTGTCT**-----ATAC-----

Ba06 AATACAA**AGCTTATC**AAAGAG-**AGGCGGAAGGA-CITGG-CCC**TTTGA**AGCC-CAGCAACCTGTCT**-----ATAGA-----

Ba07 TGAACCT**CTTATC**AAAGAG-**AGGCGGAAGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----GATTTA-----

Ba08 AAATTAAT**TTCTTATC**CAGAG-**AGGTGGAAGGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----AAAT-----

Ba09 ATGAAA**TTCTTATC**AAAGAG-**AGGTGGAAGGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----TTA-----

Ba10 GAATAT**TTCTTATC**CAGAG-**AGGTGGAAGGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----GAT-----







Ba11 TATACAA**CTCTTATC**AAAGAG-**GGTGGAGGGA-CITGG-CCC**GATGA**AGCC-CAGCAACCTGTCT**-----GTAATAC**CTGTGAATGGGGCTTTATCAGGCCA**

Ba12 TAAATA**CTCTTATC**AAAGAG-**GGTGGAGGGA-CITGG-CCC**GATGA**AGCC-CAGCAACCTGTCT**-----TAAT-----

Ba13 ACGAACA**TTCTTATC**TAGAG-**AGGTGGAAGGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----ATT-----

Ba14 AAGACA**CTCTTATC**TAGAG-**GGTGGAGGGA-CITGG-CCC**TATGAC**ACCT-CAGCAACCTGTCT**-----GAAAT-----

Ba15 GGATACTCTCTATCCCGA[CT][GGG]GGAGGGGACAGGCCC[CATGAAAGCC][GAGCAACCTCACATTCTA]-----GTGGTAAA-----
Ba16 CTGATTTCCTTATCAAGAG[CA][GGT]GGA[GGG]AC[TTG]GCCC[GTGTAAGCC][GGGCAACGGTCAAG]-----TTAT-----
Ba17 TTGCATAGTCTTATCAAGAA[AA][AGG]TGAAGGGA-CAGGCCC[GATGAACCC][GGCAACAGCCCGT]-----ATA-----
Be01 CGATACA[TTCTTATC]CAGAG[AGG]TGAAGGGA-CTGGCCC[TACGATACCT][GAGCAACGGGTT]-----TTTT-----
Be02 CAACAA[TTCTTATC]TGTGAG[AGG]TGAAGGGA-CTGGCCC[TATGAACCT][GGCAACCTCGT]-----ATGAG-----
Be03 AATACAAAGCTTATCAAGAG[CA][AGC]GGAAGGGA-CTGGCCC[GGCGAAGCC][GGCAACCTGGCT]-----ATAGA-----
Be04 TGAAC[CTTCTTAT]TAAAGAG[AGGC]GGAAGGGA-CTGGCCC[TACGATGCCCT][GGCAACGGGACTG]-----GATTCA-----
Be05 AAATTAA[CTTATC]CAGAG[AGG]TGAAGGGA-CTGGCCC[TATGAACCC][AGCAACCCCTATA]-----TATATT-----
Be06 ATGAAA[TTCTTATC]ACGAG[AGG]TGAAGGGA-CTGGCCC[TATGATACCT][GGCAACGGGATTCG]-----TTA-----
Be07 ATTAG[TTTCTTAT]TAAAG[AGAT]GGAAGGGA-CTGGCCC[GATGAACCT][GAGCAACAGGCT]-----ATAA-----
Be08 GAATATTTTCTTATCAGAG[CA][GGT]GGAAGGGA-CTGGCCC[GATGAACCC][GAGCAACGGG]-----GAT-----
Be09 TAAATA[CTTCTTATC]AAGAG[CA][GGT]GGAAGGGA-CTGGCCC[GACGAACCC][GGCAACGGGATCTAG]-----AATT-----
Be10 AGACAAA[CTCTTAT]TGAAG[CC][GGT]GGAAGGGA-CTGGCCC[GTGTAACCC][GGCAACGGTCAAAAG]-----GAAAT-----
Be11 ACGAACAC[TTCTTATC]TAGAG[AGG]TGAAGGGA-CTGGCCC[TATGACGGCT][GAGCAACGATTAAAG]-----ATTT-----
Be12 TATACAA[CTCTTATC]AAGAG[CA][GGT]GGAAGGGA-CTGGCCC[GATGAACCC][GAGCAACCGAGCC]-----GTAATA[CCATTGTGAAATCGGGCGT]TTATTT[ACGGCC]-----
Be13 GGATACTCTCTTATCCGAG[CT][GGC]GGAAGGGA-CTGGCCC[GATGAAGCC][GAGCAACCTGACTTGT]-----ATTGGTAAAC-----
Be14 CTGA[TTTCTTATC]TAAAGAG[CA][GGT]GGAAGGGA-CTGGCCC[GTGTAACCC][GGCAACGGTCAAG]-----TTTAT-----
Be15 TTGCATAG[TTCTTATC]AAGAG[AA][AGG]TGAAGGGA-CTGGCCC[GATGAACCC][GGCAACAGCCGT]-----ATA-----
Be16 TTTA[CTCATTTGATC]AAGAG[AGG]TGAAGGGA-CTGGCCC[TTTGAACCC][GGCAACAGGTTCA]-----TTTT-----
Be17 ACACATA[CTCTTATC]AAGAG[CT][GGC]GGAAGGGA-CTGGCCC[GATGATGCC][GGCAACGGAGCTTATA]-----ACG-----
Be18 AGCAATTTACTTATCAGAG[AGG]TGAAGGGA-CTGGCCC[TATGACACCT][GAGCAACGGGTTCT]-----GTAATA-----

							
Cons	r. GTGCYaa.i-Cc.r-----carr-----yyIgrnGATRagrr.rr-----						
Bs01	-----GCCATGACCAAGGTGCTAAAT- CCAG -----CAAGCT-----CGAACA-----GCTTGGAAAGATAAGAAAGAGACAAAATCACTGACAAA-----						
Bs02	-----GCAAAAGCGCAAAGGTGCTAAAT- CCAG -----CAAGCGT-----TTTTT-----ATGCTTGGAAAGATAAGAAAGAACGCTTAAA-----						
Bs03	-----TGATGTCTCATAA-----GGCACGGTGCTAAAT- CCAT -----CAGAT-----TGT-----GTCGTGAGAGATGAGAGAGGCGAGTGTTTTACGTAGAAAA-----						
Bs04	-----GCTGCTCTCTAA-----GGCACGGTGCTAAAT- CCAT -----T-CAGAT-----CTG-----ATCTGACAGATAAGAGAGGCGGACATAGATGTTAA-----						
Bs05	-----AAGCACGGTGCTAAAT- CTTG -----CAGCT-----AGC-----GGCTGAGAGATAAGATTCGGACGAGAGAAACGAAA-----						
Bs06	-----JGTAAAGGTGCT-ACT TCCAG -----CAAATG-----AATTC-----CATTTGAAAGATAAGGGCTGCAATGCTGTCTCCTGT-----						
Bs07	-----JGTGCCAAT- CCAG -----CAAAGC-----GCTA-----GCTTGAAGATAGGAAAAGCAAGGTTTATACCGGCGTCTGCCTG-----						
Bs08	-----GAGACAACCAAGGTGCTAA----- CCTC -----TTCCAAGG-----TTGTATCATT----- CCCTGAGCGGATAAGAGATG AAAAGGCAAAAGACCA-----						
Bs09	-----GTTCAAAATGGTGCCAAAT- CAGA -----CGAAGC-----GTTCA-----GCTTTGAAAGATGAGAGAGAAAGGCATTTTATATA-----						
Bs10	-----AACAGAAATGGTGCTAAAT- CGTT -----AAGAAC-----ATTGC-----GTCTTGCAGATGAGGCGGAGATTGTATCGTTCAA-----						
Bs11	-----ACAGAAATGGTGCTAAAT- CGTT -----TAGACAA-----TGA-----TTGCTCTTGAAGATAAGGTTGAGATTGTACACGCAA-----						
Bh01	-----AAAGAAAGGTGCCAAAT- CCAG -----CAGAACA-----TGA-----TGTTGTGAAGATAAGAAAGCGAACGGATCG-----						
Bh02	-----AGCAAACGAAGGTGCTAAAT- TCAG -----CAGAAATG-----ATT-----CATCTGTGAAGATAAGCGCAAGCGCAAAA-----						
Bh03	-----JGTGTGTCAGGTGCTAAAT- CGTG -----CAAGCA-----TTATT-----TGCTTGAGAGATAAGAGGAAAGCGAGTGAGATCCAA-----						
Bh04	-----AGGTGAAAAGGTGCTAA----- CCTC -----CAAGGC-----GTT-----GCCTTGAAAAGATAAGAGCGGAAAGGTATGTTAATTAA-----						
Bh05	-----GCTTGGAAAAGGTGCTAAAT- CGTG -----CAAAAGC-----GAT-----GCTTTGAGAGATGAGAGAAAGGGAAGACGTAAACATT-----						
Oi01	-----AGGTATGGTGCTAAAT- CCAA -----TAGGCT-----TACA-----AGCCTTAAAGATAAGAAAGACCTATGTATTTTAA-----						
Oi02	-----TAAGTACTGTGCCAAAT- CCAG -----TAGCG-----TAAT-----TGCTAGAAAGATGAGAAAGAGTATATAGTACGGTTTCTCTGT-----						
Oi03	-----JCTGTGCTAAAT- CGTG -----CAAGC-----ATA-----GCTTGAAGATAAGTTGAGGTTATCGTAAATATCCAAGTTCTCT-----						
Oi04	-----GGAGTGGTGCT-TC TCCTG -----CAGAA-----TTTT-----TTCTGAAAGATAAGGTAAATGATATGTAAAA-----						
Oi05	-----GGTGAAAAGGTGCTAA----- TCCTG -----ATGCAAGGA-----TAATAGT-----TCCTTGAACATAAGAGCGCAAAAGGCCATAATTCTT-----						
Oi06	-----ATGAAAGGTGCCAAAT- CGTG -----CA-----GAAA-----TGAAAGATGAGAGAACGTCAGACGATATACGATAAAATACG-----						
Oi07	-----AGAACTACTGTGCCAAAT- CCAT -----CAAGCA-----AAT-----TGCTTGAAGATAAGAGT-----AGAAATAATTATTACCTTTAAAA-----						
Oi10	-----GAATACTGTGCCAAAT- CCAT -----CAAGTAT-----TCT-----ATGCTTGGTAGATAAGAGAAAGTCCGCGCACAG-----						
Oi08	-----GTAACTACTGTGCTCAAT- CCAG -----CAAGC-----GTAG-----GCTTGAATAGATGAGAAAAGTGTTTATACCTTTTAAATAAAA-----						
Oi09	-----GCTATTGAAAGGTGCTAAAT- CCTA -----CAGAC-----TTCATC-----GTTCTGGAAGATAAGAGGAGGTTCCGGTTTAAACAGACAAA-----						
Oi10	-----GAATACTGTGCCAAAT- CCAT -----CAAGTAT-----TCT-----ATGCTTGGTAGATAAGAGAAAGTCCGCGCACAG-----						
Oi11	-----TAGAAAGGTGCTACCT- CCAG -----CAAGAT-----GTAT-----GTTCTGAAAAGATAAGAGTCCAGATTAAAAA-----						

O112 -----TAAAGAAATCTGTGCTAAAT-**CC**TG-----CAAAATGC-----AAACGA-----GCATTGTGAAA**CATGAGAAA**CGATGGCTTCTACATATATACATATG
 O113 -----GTGATGAATAGGTGCTAAAT-**CC**TG-----CAAAATAG-----GGACA-----GTATTTTGAGAAA**TAAGAGA**GGTGATGAATGACTTACGTAGTGTA
 Ca01 -----TTGGAGATGTGCTAAAT-**CC**TA-----CAGG-----TTTAT-----CCTGAC**AGATGAGAA**TGTTTTTAAA-----
 Ca02 -----AATATATCTGGTGCTAAAT-**CC**TG-----CAGC-----AAAC-----GCTGAT**AGATGAGA**TAAATCGCGAATGTAAA-----
 Ca03 -----ACTTATGTGTGCTAAAT-**CC**AG-----CAGGA-----TAAT-----TTCTGAAA**AGATGAGGAG**CGACTATTTAAACAATTTTATTTTGT
 Ca04 -----TATACAAAGGTGCTAAAT-**CC**TG-----CAGC-----GCTA-----GCTGAC**AGATGAGA**TATAAATCGAGCTTTA-----
 Ca05 -----GTACGGTGCTAAAT-**CC**TG-----CAAAAC-----TTATTT-----GTTTGA**AA**CA**TA**TA**AGAAA**ACAGCTTATTAAATGAGTATGT
 Ca06 -----AGATGATAGGTGCTAAAT-**CC**TG-----CAAG-----TTAA-----TTTGTAG**AGATAAGAG**GGATTATAAAATTTTAGAAAGCTAAAA-
 Ca07 -----AGTACATAAAGGTGCTAAAT-**CC**TG-----CAGAA-----TTA-----TTCTGCA**AGATAAGAG**AGAGAAATGTTAA-----
 Cp01 -----TCACACGGTGCTAAAT-**CC**GG-----TAAAGA-----AAT-----TCTT**TA**CAAG**ATGAGAG**AAAGATAAATTTAGTGATAACTAAAA-
 Cp02 ATTTCTCTATGCAAAAGATTTATAGCGGTGCTAAAT-**CC**TG-----AGAA-----AGTGA**CA****TA**TA**AGAA**AGAGAGCTGTGTAAGAAATAATA-----
 Lm01 -----GTTCTATGCTAAAT-**CC**GA-----CAGAA-----GTAATA-----TTCTGGCA**AGATAAG**ATAGTAGCTTTTCAATGAGG-----
 Lm02 -----ATAAAGTGAAGGTGCTAAAT-**CC**AG-----CAAAATGG-----TGTATT-----CCGTTTGGT**AGATAAGAGGAG**CTGGATATGTTTCGACTTTCC-----
 Lm03 -----TTTCAAGGTGCTAAAT-**CC**AG-----CAG-----TATATT-----CTGAAA**AGATAAG**TCGGAAATCCAAATTTAGGAAACTCTAT-
 Lm04 -----TCACGGTGCTAAAT-**CC**AG-----CAG-----GTAACA-----CTGAC**AGATAAG**CCACCGGAATCAGGTAATTTACT-----
 Lm05 -----GTGAAAGGTGCTAA-**TC**TG-----TTGAGGAG-----TATTAT-----CTTCTGA**ACGATGAGAG**CAAAAGTATAATTAT-----
 Lm06 -----TTGAAAGGTGCTAAAT-**CC**TG-----CGAAGTG-----TGA-----TGCTTCGAGAG**ATAAGAGAGAG**ACTTAAAAAGTTTCAGTGATTTGT
 Lm07 -----TTATCTGTTTAAGGTGCTAAAT-**CA**TG-----T-CAGAA-----CTAA-----TTGTTCTGA**AGATGAG**AGGAAAGTTAGTCCATTTGAAAAAATGCT
 Li01 -----GTTCTATGCTAAAT-**CC**GA-----T-CAGAA-----GTAATA-----TTCTGGCA**AGATAAG**ATAGTAGCTTTTAAATGAGG-----
 Li02 -----GTAAAGTGAAGGTGCTAAAT-**CC**AG-----CAAAATGG-----TGTATT-----CTGAAA**AGATAAG**TCGGAAATCCAAATTTAGGAAACTCTAT-
 Li03 -----TTCAAGGTGCTAAAT-**CC**AG-----CAG-----TATATT-----CTGAA**AGATAAG**TCGGAAATCCAAATTTAGGAAACTCTAT-
 Li04 -----TCACGGTGCTAAAT-**CC**AG-----CAGT-----ATC-----ACTGAC**AGATAAG**CGCACGCGAAACAGGTAATCACT-----
 Li05 -----GTGAAAAGGTGCTAA-**TC**TG-----TTGAGGAG-----TAATAT-----CTCTGA**ACGATGAGAG**CAAAAGGTATAATTATA-----
 Li06 -----TTGAAAAGGTGCTAAAT-**CC**TG-----CGAAGTG-----TGA-----TGGTTGGAG**AGATAAGAG**AGACTTAAAAAGTTTCAGTGTATTTGT
 Li07 -----TTATGTTTAAAGGTGCTAAAT-**CA**TG-----CAGAACAA-----CGAT-----TTGTTCTGA**AGATGAG**AGGAAAGTTAGCCATTTGAAAAAATGCT
 Sa01 -----AGCACGGTGCTAAAA-**CC**AA-----CGAG-----TTA-----CTCGAAT**AGATAAG**TATAAAGA-----
 Sa02 -----GAAATGGTGCTAAAT-**CA**CA-----TAAAGT-----TTTA-----ACTTTTGA**AGATGAGAG**AAACAATACTACTAT-----
 Sa03 -----AAAAAGAAAGGTGCCAAA-**CC**GT-----TTGCAGAC-----AAATAG-----GTCG**AA**CA**AGATAAGAG**CGGAATGGAGGTATTA-----
 Sa04 -----ATTGTGCCAAT-**CC**AG-----TAAACG-----TAA-----TGGTTTGA**AGATAAG**CAAGGTAAAGCACATGA-----
 Sc01 -----CCGGCTAGGGAAGGTGCCAAT-**CC**GT-----CTCAGGGG-----AGATG-----CGTCTG**AGAA**CA**ATGAG**AGAGAAAGGGCCCTCGCTCCATGGCTGTGC

	P3		Cons	P4		Cons	P5		Cons	P6		Cons	P7		Cons	P8		Cons	P9		Cons	P10		Cons	P11		Cons	P12		Cons	P13		Cons	P14		Cons	P15		Cons	P16		Cons	P17		Cons	P18		Cons	P19		Cons	P20		Cons	P21		Cons	P22		Cons	P23		Cons	P24		Cons	P25		Cons	P26		Cons	P27		Cons	P28		Cons	P29		Cons	P30		Cons	P31		Cons	P32		Cons	P33		Cons	P34		Cons	P35		Cons	P36		Cons	P37		Cons	P38		Cons	P39		Cons	P40		Cons	P41		Cons	P42		Cons	P43		Cons	P44		Cons	P45		Cons	P46		Cons	P47		Cons	P48		Cons	P49		Cons	P50		Cons	P51		Cons	P52		Cons	P53		Cons	P54		Cons	P55		Cons	P56		Cons	P57		Cons	P58		Cons	P59		Cons	P60		Cons	P61		Cons	P62		Cons	P63		Cons	P64		Cons	P65		Cons	P66		Cons	P67		Cons	P68		Cons	P69		Cons	P70		Cons	P71		Cons	P72		Cons	P73		Cons	P74		Cons	P75		Cons	P76		Cons	P77		Cons	P78		Cons	P79		Cons	P80		Cons	P81		Cons	P82		Cons	P83		Cons	P84		Cons	P85		Cons	P86		Cons	P87		Cons	P88		Cons	P89		Cons	P90		Cons	P91		Cons	P92		Cons	P93		Cons	P94		Cons	P95		Cons	P96		Cons	P97		Cons	P98		Cons	P99	
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Ba15 -----TACAGGTGAATAGGTGCTAAAA-**CCTC**-----TG-**CGAGGCT**-----ACA-----GGTCTCGAACGATAAAGAGCGAAGGCGCAAAAAAGCAGTATGCAAGTA
Ba16 -----GTTGAAATGGTGCCTAATT-**CCTC**-----CAAAGC-----AAATG-----CTTTGAGAGATGAGAGAGAGCGATAATGTTGTTATATACGCAT
Ba17 -----ACGGAATTGTGCCAAAT-**CCTC**-----CAGG-----TAATAAAT-----CCTGAGAGATAAGAAAGAGCCTTTAGAGCGTGTGTTTCAAA--
Bc01 -----AATACCGTGTCTAACT-**CCAG**-----CAAGCT-----ATGAA-----AGGCTJGGAAGATGAGAGATGTGAAACGAGTACATATAA-----
Bc02 -----ACGAAAGGTGCCAAAT-**CCTC**-----CAGGTG-----AAGAAA-----CACCTGAAAGATAAGAGCGGTTCAAATTAGTCAAGAAAG-----
Bc03 -----AAGCAAGGTGCTAAAT-**CCAG**-----CAAAATGG-----AAT-----CCATTTTGAAAGATAAGGTAAATATATACCGAACAG-----
Bc04 -----CAGTCTGTGCCAAAT-**CCAG**-----CAAGC-----ATAT-----CCTTGAAACATGAGAAAGAGCGTTTCTTATAGATGTATAA-----
Bc05 -----TATAGGAAAGGTGCTAATT-**CCG**-----CAGAGAACAC-----GAT-----GTGTTTTTGGAAGATAAGAGGATTCCTGAAACGTGAAAGAAAA-----
Bc06 -----TGAATACTGTGCCAATT-**CCAG**-----CAAG-----GTAA-----CCTTGAANAAGATAAGAAAGAGCTCAITTTGACTGTATATGCAG
Bc07 -----AGTACTGTGCTAAGT-**CCAG**-----CAAAGCT-----ATGAA-----GGTTJGGAAGATGAGGGGAAATGGATTAAACATTCAA-----
Bc08 -----GCAGGTGCTAATT-**CCAG**-----CAGAACA-----TATT-----TGTTCTGGGAGATAAGACGAAAGATATATACGTAA-----
Bc09 -----GTAGACACGGTCTAATT-**CTCG**-----CAGC-----ATTAC-----GCTGACAGATAAGGAGCTGTGTTGTAAAAA-----
Bc10 -----GTTTGAAACGGTCTAATA-**CCTC**-----CAAAAG-----GAAT-----GTTTGCATATAAGAGGAGGATCGATTATGT-----
Bc11 -----GTTAAATAAGGTGCTAATT-**CCAG**-----CAAAAT-----GTGAAA-----GATTGACAGATGAGAGAAAGAGCTCTATTCAAACCGAAA-----
Bc12 AAAA-----GGCACGGTGTCTAATT-**CCAG**-----CAGAAAAGT-----AAA-----ACTTCTGCGCAGATAAGAGGGGAGAGATAAACTTCAA-----
Bc13 -----ACAAGTGAATAGGTGCTAAAA-**CCTC**-----TG-**CGAGGCT**-----ACA-----GGTCTCGAACGATAAGAGCGAAGGGCAAAAAGCAGTATGCAAGTA
Bc14 -----GTTGAAATGGTCCCAATT-**CTC**-----CAAAGC-----AAAT-----GCTTTGAGAGATGAGAGAGAAAGAGCCTTTAGAGCGTGTGTTTCAAA--
Bc15 -----ACGGAAATTGTGCCAAAT-**CCTC**-----CAGG-----TAATAAAC-----CCTGAGAGATAAGAAAGAGCCTTTAGAGCGTGTGTTTCAAA--
Bc16 -----TGAATACTGTGCCACTT-**CCTC**-----CAAGCT-----TTAT-----AGCTTGAAAGATAGAAATGAGGGGACTTCGTTTATATACGGGTGCA
Bc17 -----TATAAGCTAAGGTGCTAATT-**CCTC**-----CAAAACGA-----GTTT-----TCGTTTTGGAAGATAAGAGAGGAAATCTATTTTGTCTATTG-----
Bc18 -----GGAAACAAGGTGCTAATT-**CCAG**-----CAAG-----CAAGT-----CTTGAAGATAAGTATGGGCTTTGTTTATTA-----

ConsT----->	<-----T-----mmr..tftty.....
Bs01yyyy.....GTCCTCTT.....AAGGACCTTTTAACTCTCTTTTCCCTGCTGATGTGAATAAAGGAGGCAGACA ATG
Bs02CCCTCTCTTC.....TTAT.....GAAGAAGGGTTTATTTTGAAAGGGAAGGTGTACAGCTAT ATG TCACACGACGTTGAAA
Bs03GCTCTCTCTC.....TCAT.....GGGAAAGAGGCTTTTGTGTGAGAAAACCTCTTAGCAGCCTGTATCCGCGGGTGAAAGAGA
Bs04GCCTCCTCTC.....TCT.....GAGAAGGAGGCTTTTACGGCCACATATTAAATTAAATTACATAAATTGGAGGTT ATG ATGATG
Bs05CCTCTTTAGACGC.....GATT.....GCAGTTTGAAGAGGTTTTTTGAT ATG GATGAAAAATGAAAGGAGCTCTGGCATGAGTGAGTTATTA
Bs06CTTCTCTCC.....GCC.....GGATTGAAAAGTTTTTTTATTTTAAAGGTTAAAAAGGCTATCTGTATATCAGCAGCCCGGAAT
Bs07	TAACAGAGCGCGCTATATGAATCTCTTCC.....ATCTTC.....GGAAAGAGATTTTTTTT ATG AAAAATACGATGAAAAGGATGTTTTTGCGCATGACGGTTTT
Bs08CCCTTTTCC.....TCGAT.....GGAAAAGGTTTTTTTATTTTCATAAATAAGCCAAATTACATCTCTAATAATAACTGTACA
Bs09GCCTTTCTGC.....TCAAGTGT.....GCAGAAAGGCTTTTCTTTTGCAGAAAAAACCGGAAGATTCTCTTAGAATAGTGTAAAGGCAG
Bs10GCTCTTCTCT.....ACACA.....AAGGAAGAGCTTTTACATGCTTAATAATTCAGAAAAGAGGCGAAATAAC ATG GCTCAACAA
Bs11GCTCTTCTCT.....ATCCA.....AAGGAAGAGCTTTTATATTGAATGGAAAGAAAGGAATGGACAACATGTCACAACAAACA
Bh01CACGCTCTC.....TTATC.....GAAGAGGTTTCTTTCTTTTAAACCTTTATCTGTCGGAAAGATTACTTGTATTGTGA
Bh02CCTTTCC.....TTATC.....GGAAAGGTTTTTTGTAGAGAGCCAAAGTTTTTATAAAAAATGAGGAGGGCATACGA
Bh03CACTACITCTCTCT.....AATCTTACATGAC.....GAGAAGGTAGTGTTTTTTTACACAAATCAGAAAAGATCGAACTTTTCAGATAGTTTAAGAAAAA
Bh04CCCTTTTCC.....TCATAAT.....GGAAAAGGTTTTTCTCTAATTTTATCTTTTGCAAGTGTCTGTGGAGAAATGAGTGCCGT
Bh05CCTTTCTGC.....TCATG.....GCGGAAAGGTTTTTTTGTCTCTAATATGCAGTTGATTCACGGAAATTGTACTTTCTTACGA
Oi01CCCTCTCTCT.....TACTTTT.....AGAAGAGGGTTTTTTGATTTTGAATAGGAGGAGATTAT ATG AAGCGGAGTTTACAAA
Oi02CCCTCTCTCT.....TACTTGT.....AGAAGGGGTTTTTACTTTTCCCTATCTCTGTACAGAACTGTCTATATGCTAGTTTCATA
Oi03	CTTCTTATCTTTATCATGTTTTTT.....AATAGAAGGGATGGATTATAT ATG AGCATACGGAAATGAAGATGAAACGGA	
Oi04CCCTCTCTCT.....GAAAT.....GAAAGAAAGTTTTTTTGTATGGGAT GTG TTATGTATGATTCAGTTGGAAAAATATCGAGAA
Oi05CCTTTCTCAT.....GTT.....ATGAAGGAAAGGTTTTTTTGTTTTATCTATAATTTTAGTACCGCGTTTTTTTAGTACGAGGT
Oi06	TA.....CGTCTTTCTGT.....TCTCTT.....ACAGAAAGGGTTTTTATTTTGACGAATTAATGGGAAACTATACGAAATGGTTGCTGGAGAG
Oi07CTCTATCT.....TATTAC.....GGAATAGAGTTTTTTGTACATAAGATGGCTCTATAATATTTGTGGGTAAAGAAAAA
Oi10CTCTTTCTTA.....TCTT.....TATGAAAAGGTTTTTTTAAATTAATAACGATAGATAATCGGGGATGAAA ATG AAGTATGGTTT
Oi08CTCTTTC.....TCATC.....GGAAAGATTTTTTCTTTGTGTGAGGGTTTGGAAAAATAAGTGGAAACAGTTTGA
Oi09GTCTCTCTC.....TTAT.....GAAGGGGCTTTTTTTTAAATCTCTCTTATTACTTTAAAAATAATAATCAAGGAGAA
Oi10CTCTTTCTTA.....TCTT.....TATGAAAAGGTTTTTTTAAATTAATAACGATAGATAATGGGGGATGAAA ATG AAGTATGGTTT
Oi11TCCGGACGCCTTA.....TTTAT.....TAAGGGCATCGCGGATTTCTTATATTAAATTTTAAAGGAGATTGGTAA ATG AACAACAT

Oi12	GTACGAA-----TCCTCTTTTCTTG-----TCITT-----CAAGAAAAGAGGGATTTTTTTATTTCGCTTGGGGTTGAGACA ATGA ATTGAATTCAGAAATGTAACA
Oi13	TGTTA-----TGCCCTCGAT-----TTCAC-----ATCGGGAGGCATTTTTTAGTTTCCCGGAAAAATTCACAACATGAGAAAAAGGAGGATTT A
Ca01	-----CTGCTTCTATT-----TTTAAT-----GGATAAGAAGCAGTTTATTTTTTTATTATTAGGAGGAGAAAGATT ATG GGAGAAATAGATTGTA
Ca02	-----GCCGAGG-----TTATTT-----CCAAGGCTTTTTTATTATCTCATTTTTTAAAGGGGCTAACT ATG AATCTTCACTA
Ca03	TAATAGA-----TCCTCTCTT-----TTAA-----AAGAAGAGGATTTATTTTGTTAATAATAGAACCAACTTATTATTATTTGGTTTATTCTTA
Ca04	-----GAGCAGAG-----TTTATT-----CTCTGGCTCTATTATTTTTTAACTAAATGGGAAAGGTGAATGCAC ATG ATAGAAAAATAAA
Ca05	AATAA-----TCCGTTTTTC-----TTATT-----GGAAAATGGATTTTTTTATATATTTAATACTAGGACGGTGAAAAAAA ATG CCTATA
Ca06	-----TCCTCTTC-----AACTAA-----GAAGAGGATTTAAATTTTATATATTTTATAGTTTATAGATATGGAATTAATAATAATAA
Ca07	-----GTCTCTTC-----TTATT-----GAGGAGACTTTTATTTTATATCTAGGAGGAAGTGGATATA ATG AGAAAGTTATTATC
Cp01	-----TCCTCTTAAATCT-----TTAA-----AGTTTGAGAAGAGATTTTTTTATTAACAAAAATTTTAAAGCCGCATTAAATAAAGTTTGT
Cp02	-----CTTCTATC-----CTAG-----GATAGGAGTTTTTATTITGTAGGATAAAGGATAGATTTTATTAAATGGATTAGGAGGA
Lm01	-----TGCCTCGATCTG-----ACCAAAAA-----CAGAGGAAGCTTATTTTTTTAGCGCTTAAAGAGGGGAGTTTTTGT ATG AAAGAAATTTT
Lm02	-----ACTTCTATT-----CTAA-----AATAGAGAAGTTTTTTTTATGCTTTCATGAATAAATCTGGATAATCACACACATACCTAGG
Lm03	-----CCCTCTGGCG-----CTTATATA-----CTGCTAGGAGGTTTTTTTGATGGAAATTA CTG ATAAATACATATCAAAGAGGAGTGGATTT A
Lm04	-----CTTTCCCTTAAAG-----CTGT-----CTTTAAGGAAAGTTTTTTTATACATAAAAAATAATAAGAAITTGAGGCGAAGAAAA ATG AACCAAG
Lm05	-----AGCCTTCTCTATCTGCGCGGTTTT-----GTGCAAAATAGAGAGAGGCTTTTTATATGAGACGTATTTGGAGAGAAATTGAAGGAGGAAAAATAAAA ATGG
Lm06	GATCGAAACTTCCAAA-----CCTCTCTAG-----TTCT-----CTAGGAGGTTTTTTTATTGGCAAAAAATCGAGAGGATAAGGTGATAGT ATG GTAAGGC
Lm07	-----GCCTTCTGCT-----CATC-----AGCAGAAAGGCTTTTTTTTGATATACAGAAATGTAGAAAAGGTGATAGAG ATG ATTACGTTACA
Li01	-----CGCTTCGATTCTG-----ACCAAAAA-----CAGAGGAAGCTTATTTTTTAGCGCTTAAAGAGGGGAGTTTTTGT ATG AAAGAAATTTTAA
Li02	-----CTTCTCTATT-----CTA-----AATAGAGAAAGTTTTTTTATTCCTTTCATGAATAAATCTGGATAAATAATCAACATACTAGG
Li03	-----CCTCTCTGGCG-----CTTATATA-----CTGCTAGGAGGTTTTTTTGATGGAAATTA CTG ATAAATACATATTTAAAGAGGAGTGGATTT A
Li04	-----CTTTCCCTTAAAG-----CTGT-----CTTTTGGGGGAAAGTTTTTTTGATACATAAAAAATAACTAGAAATTGAGCGGAAGAAA ATG AAATCAAG
Li05	-----GCCCTTCTATCTGTCGCG- TTT -CGTGCAAAATAGAGAGAGGCTTTTTTATATGAGACGTATTTGGAGAGAACTAAAGGAGGAAAAATAAAA ATGG
Li06	GATCGAAACTTCCAAA-----CCTCTCTAG-----TTCT-----CTAGGAGGTTTTTTTATTGGCAAAAAATTCAGAGGATAAGGTGATAGT ATG GTAAGGC
Li07	-----GCCCTTCTGCT-----CAAT-----AGCAGGAAGGCTTTTTTGTATATCAGAAATGTAGAAAAGGTGATAGAG ATG ATTACGTTACAG
Sa01	-----CTTCTTACTTT-----TCAAT-----AGGCTGAGAAGTTTT TG TTTAAGGAGGAAAAAGCAATGACAAAATTACACAGTAGATACTT
Sa02	-----TGCCTTCTCAATTTT-----TCTATC-----GATATGAGAAAGCATTTTTTATTATTAAGCAACACAGGGAGGAATCAAC GTG ATTGAATTAATA
Sa03	-----GGCCTTCTCTCTAT-----ATTA-----ATAGTTAGAAGGCTTTTTTATTATAGCTCACAGAGAGAAATTTTCGTAAATATAAATTTAAAGGA
Sa04	-----ACCTCTTCTTCA-----TCGTT-----TGTGAGAAAGAGGTTATTTTAAITGGAAAGCAGTAAAAAGGATGGAAGTACATAAAAGAGCA
Se01	AGACTGCCGAAACCTCCACGAACC-----CCACCGAGCCCGCTCGACCTCGCCCCCGCCACCCGCGCTGAGCTGCCGGG

	-----T----->	<-----T-----
Consyyyyy.....TTTTT.....
C101	CTTGAATGCTTCCCGCAGATACCTCTGACCCCGACCGGCACTACGGATCGAGGCTTCAACCTTGTACCATTTGCCA	ATGAGTGAGGATAACACCTTCCGGTTCGAGACCTTGCAGGTTTCAC
T101	-----CCCTCTCT-----TTT-----	AGAAAGGGTTTATATTTTGCCTTAAGGAGGAAGAAATGCGTAGACTCTTTACTTCTG
T102	-----GTCTCTTC-----TTTTAGC-----	GAAGGGACTTTTATTTTAAATAAAGAGGGGCATTAATATGTTGAAAAATGAAAAGCT
T103	-----TTACTAGGCCCTCTTC-----TCATT-----	GAAAGGGCCTAAGAAATTTCTCGAGGTGCAAAAATGAGGGTAAAGATTGGGTTGATGGGACTTTGGA
F101	-----CTCTATCT-----GGAAAT-----	GGATAGAGTTTATTTTAAATATTTTGTAAATTTTAAAGGAGGAAAAATGAAAAA
F102	-----TCCATACT-----CTATAA-----	GGTATGGAATTTTAAATTAAGTAAGAAATTTATATAGAAAGTAGGGAATAAATATGATTAT
D101	CGGACGGCTCAGCCC-----TGGCGTGCCCTTCCAGACTTC	TTTCGTCCAGGAAGGGGACGCCGTTTGGGCCGACCTCTCCGCTCTCCCCACCGAGGCCGCCGCCGTTGACCTT
D102	CATCACCCAGAGCGTCGGCTTCC-----GCCAA	TCCGTCCATCAACCATCAACCGTCCACCATCACCGAGGCCGCCGCCG
Xa01	GAGCTCC-GCGAAGCTCGATGGCC-----	GATCCACCCCTGGATACCGCCATGAGCCCTCGTGAATACTGCAATCGCCGTCTA
Xc01	GAGCTCCCGCGAAGCTCGATGGCC-----	GATCCACCCCGGATATCGGCCATGAGCCCTCGTGACACAGCATCGGCCACTCA
Se01	-----GTGCCCTTTACATC-----AATT-----	GAGTAAGGCACCTTTTATTTGAAGGAGGTAGGAACATATTATGACGAATTACACGGTTAATA
Se02	TATCTATA-----	
Gs01	-----GGCCCCCTTCCCG-----TTTCC-----	CGGAGAGGGGCTTTTCATTTTCGCCGCCCGCGCACCGGCCCTGGGGAAATCATGTCCGTCGG
Gs02	A-----TCCTCTTCCG-----CACCC-----	CGGAAGGGGATTTTTCATGTGGAGGAACCATGAACATCCGACGCGCAGCACAGATC
Ba01	-----GCACCTCTC-----TTATTTT-----	GAGAGGTGCTTTTATTTTGGAAACATATATGAAGGGGAACTATAGATGAATAAAGTATTT
Ba02	-----GCCTTGATCTTA-----TTTTT-----	TAGGATCAAGGCTTTTGTATCTAAAGAGAAAAAGGGAGTAATGGAATAAGTACGTTTCATA
Ba03	TAACTTGTACGTAAAAA-----TCCCTCTTCTC-----AATAC-----	GAAAAGAGGGATTTTATTTTTCATTTCCCTCATCATATCCAACTTAATTATTAGGAG
Ba04	-----GTGCTCTCCTTCTTATC--TTATGGTT--	GATAAGAGGAGAGACACTTTTATTTTACCTCGAGAGCTCTACTTCAAGTTTTTACAGCATATAGGAG
Ba05	-----CTCATCTTTTC-----TTGATCAT-----	GAAAGGTGAGTTTATTTATTTCAAAACATATATTGGAGGTATTTAAAAATGAAGTAATT
Ba06	-----TCCTTTTC-----GAAATG-----	GGAAGAGATTTTATTAAGAAATAAAAGGGGGCTGTTCCGCTGAGCGTACGGGAACAT
Ba07	-----GACCTCTTCT-----CGTT-----	GGAAGAGGTCTTTTGTATTTCAATTAGAAAAAAGGTTGAACACTAGGGAGAGATGGTACTTTTG
Ba08	-----TGACCTCTT-----ATGT-----	AAGAGGTCAATTTTGTGTATAGAAAAGGGAGTGTGATGCATAATTCAATTTTCAAAATA
Ba09	AA-----GCCCTTTCTA-----TCCTT-----	TAGAAAGAGGCTTTTACGTGAAAAATAAAGGAGGAAGAAAAATGGGAGCGCAGGAGTAG
Ba10	-----CTTCTTTC-----TTATC-----	GGAGAGGTTTTTTATGCAAAAAAACCGATTACGAAAAAATTTATATTAAGAAAGAAA
Ba11	-----CCTCTTCT-----TAGT-----	GGAAAGAGGTTTTTCTACGTAGAAAAAACCTCTGAATGAAAAAAGGGGGAGAAAGCAGATG
Ba12	-----CCTCTC-----CTTAGCT-----	GAGAGGTTTTTTATTTAATTAACATAGGAGTTATAACAATGAGCGGAATTATAGCGACGT
Ba13	-----GCCTTCT-----TCCT-----	AGAAGGCTTTTATTTATTTATTTCAACTACTGGTTCAATTTTAAAAAGGAGGAATTTT
Ba14	-----CCCCCTCTCA-----AAG-----	TGAAGAGGGGTTTTTATTTATGTAGAAAAAGGGAGATTTGTGAAAAATTACTAGATTTATTG

Ba15 GCAAAATTAAA.....CCTTTCCTCT.....ATATAA.....AGTAGGAAAGGTTTTTCTGTATGCTTGTGTGGGAGAAATAATGTATGTCCGAAATCTGTGGCA
Ba16 ATAAA.....CCTTTCCTGCTT.....CTCTA.....AAGCGGAAAGGTTTTTTTGTGTTTGAATGTGGAGGACATTCAAAATAATAAAGTAATGAGA
Ba17CTGCTCGCTTCTTG.....TTTT.....CAGGAAAGGGCAGTTTTTATTTCTATATAAAGAAAGGAGAAATGAGAAATGGGAGAAATCATGCG
Bc01GTGCTCTCCTCTTATC--TTTATGGTT--GATAAGAAAGGAGAGCACATTTTTATTTACCTCGAGAGCTCTGCTTCAAGTTTTACAGCATATATAGGAG
Bc02GCTACTCTTAT.....TTCCG.....ATAAGAGTAGCTTTTTTATGCTATAAAGTTAAAGGGGGCTGTTCCGCTGAGCGTACGGGAACAT
Bc03TCTTTTC.....GAAATG.....GGAAGAATTTTTTTTATGAATAAAGGGGGCTGTTCCGCTGAGCGTACGGGAACAT
Bc04GACCTCTTCT.....CGAT.....GGAAGAGTCTTTTGTATTCATTAGAAAAAGGTTGAAACTAGGGAGAGATGGTACTTTGA
Bc05TGACCTCTT.....ATGT.....AAGAGTCAATTTTGTGTATAGAAAGGGAGTGTGCGATGCATAATTCAATTTTCAAAATA
Bc06 AA.....GCCTCTTCTA.....TCITT.....TAGAAAGAGGCTTTTTTATGTGAAAAATAAAGGGGGAAGAAAAATGGGAGCGACAGGAGTAA
Bc07CTCTCTTAT.....ATGT.....GTAAAGAGAGTTTTTTTATTTAGAGGGGGGATAGAGTGAAGTTTGATGTACGTATTTTT
Bc08CTTCTTC.....TTATC.....GGAGAGGTTTTTTTATGCAAAAAAACCGATTACGAAAAATTTATATTAAAGAGAAAGG
Bc09CCTCTG.....CTTAGCT.....GAGAGGTTTTTTTATTTAACTAGGAGGTTATAACAATGAGCGGAAATTTATAGCGACAT
Bc10CCCTCTTCA.....AAG.....TGAAGAGGGGTTTTTTTATTTGATAGAAATGAGGAGATTTCTGAAATTTACTAGATTTATTA
Bc11GCCTTCT.....TCTT.....AGAAGGCTTTTTTATTTTATATTCAACTAAATGGTTCAATTTTAAAAAGGAGGAAATTTTC
Bc12CCTCTTCT.....TAGT.....GGAAAGAGGTTTTTCTACGTCAGAAAAACCTCTGAATATAAAAAAGGGGAGAGACGAT
Bc13 GCAAAATTAAA.....CCTTTCCT.....CTCTATTATGT.....AGGAAAGGTTTTTCTGTATGCTTGTGGGAGAAATAATGTATGTCCGAAATCTGTGGCA
Bc14 ATAAA.....CCTTTCCTGCTT.....CTCTA.....AGGCAGAAAGGTTTTTTTGTGTTTGAATGTGGAGGACATTCAAATAATAAAGTAGTGATA
Bc15CTGCTCCTTCTTG.....TTTT.....CAGGAAAGGGGCAAGTTTTTATTTGTATAAAGAAAGGAGAAATAAGAGATGGGAGAAATCATGCG
Bc16 TAACCTGTACGTAAAAA.....TCCCTCTTC.....TCAATAT.....GAAAAGAGGGAATTTTTTATTTTCAATTCCTCATCATCAAACTTAATTTTAGGAG
Bc17GCACCTCT.....TTATTTT.....GAGAGGTGCTTTTTTATTTTGAACGTATATTTTAAAGGGGAAATTAGATGAAGAAAGTAT
Bc18GCCTTGATCTTA.....TTTTT.....TAAGATCAAGGCTTTTTTGTATTTCTAAAAAGAGAAAAAGGGAGTAAATGGAAAAAGTACGTTTCATA

Bs01 GGGACTTT TAGAAGATT TGGAAAAGACAGGTGTTAA TCGGTGACGGCGCCATGGGGACGCTCCTACTCTATGGCA TTGACAGGTGTTT TTAGGAGGCTCAATATTTTCAAAGCCGGAGGA
Bs02 CGAAATTAGCTCAAAATTGGGAACCGTAGCGATGAAGTACGGGAACAGTAGTGCTCCTATCTATTTATCAACAGCATACCGCCACAGAGGGATCGGAGAA TCTACCGGATTTTGATTATG
Bs03 GTGTTTACATATAAGGAGGAGAAACAATGACAACCATCAAAACATCGAA TTTAGGATTTCCGAGAA TCGACCTGAACCGGGAA TGGAAAAAAGCACCTTGAAGCGTATTGGAAGGCGAG
Bs04 GGAGTCAAAAAACACCTTTATACGAAACGTTAAATGAAAGCTCCGCTGTGGCGTTGGCGGTGAAGCTTGGCCTATTTCGAAGCAAAAGCACGCTGACATGCCAGGAGATCGGAGACGGC
Bs05 CCGACATATCTCCTGACCGAACC GGAGCCGATACAGAGAAGAAAGCAAAATCGCAATTGACAGTAGGCTCTGGACTGATCTGCCCTTGTAAAACAGGAGCAAAATGCAA
Bs06 CACATTACATGGGAAAAGACAACCGGCAGAAAGCTACTGTTTGTCTCCGAAAGGAGGAAAGAAGAAATGTTTAAACGTATGATAATTGGGAAGAACCAACGATTTACATTTCCCGGAAGA
Bs07 TGGTTACAGCACCGTACAAACGAAAGGACGAAAGAGCTTTGAAACCTTGTTTGGCTCAGTTGCTTATCAATCTTGGAAAGAAACAAGGTAGGGCATATCGGGAGGATGAACCTCATTCAGC
Bs08 TTGTATAAGAGGGAGCGAGTCCGTATCATATATACAAAGGTCTTTCCGGAGGCCCTTGTGCAGGAGGAAGCAAAATCTAATGATAAAAATCGCTCGTGTATTTACATCAGAA TCTGTTACGGAG
Bs09 GTGATTGCTTTGATCAATCTTCAGGATGTTTCAAAAGTTTACAAGTCGAAACATGGAGATGTCAA TGTGTCCAAAACGCTCTCGCTTTCCATTTAAAAAAGGTGAGATTTTGTGGAA TTTATA
Bs10 ACGAATGTTGCAGGACAAAAAACAGAAAAAACACGCAAAAGCACCTTCCCGCGCGATCAATGTCGGCGGATCAAGTCGGAAGCCCTGCTAAAGATCTGAGCCCGTCAAAAAAGCGCGGTCGCAAAAAGCGCGCTGGT
Bs11 ACACCCGACAGACAAAATCACTTCAAAGAAAAAACCGCCGTTTCGGCGGATCAAGTCGGAAGCCCTGCTAAAGATCTGAGCCCGTCAAAAAAGCGCGGTCGCAAAAAGCGCGCGCGGAA
Bh01 CCGAAAAACAGCAAGACAAAAAAGAACAACTTGGAAATGAGGAGGCGTTGTACATGAAAAAATTTACGTAA TCCACGAAACAGATGAA TGGACGGTTCACTATTTAAACGACTTGAGGA
Bh02 AAGGGCAAA TAAATCAGATGAAATTAAGTTTGGTGTGATCGGATTTGGCACCGTTGGCAAGGTGTGAGAGGTCAAGTGTGAGAGGTCTAATGAAACAGCTTTAGTACAAATCGGAAATCGGAATGTC
Bh03 TGAAGGCTTTCGCAACTTGGCGACGAGCTGATTTTCCAAATAGATGGATAGGAGGAGCAACATGAAATCGTAAAGAAATTAAGAAACAGCTTTAGTACAAATCGGAAATCGGAATGGAATGATC
Bh04 ATCATGTTTTGGCGACGCTGCGTTGGTAAGGGTGTGCTTAAGGAGGATATTCGTAAATGGCAGATACAAGAGTCGTGCTTATTTACATCAGAGTCTGTTACAGAAAGGACATCTCTGA
Bh05 TAATGATTTGCGTCTCTTGAGACGAAATTTGCGAGAGTGAGAGTTTTGCTCTGCTACTGACTTTGCTTAAATTTGGTAACCGGTAGACCACTGATATATTTTAGAAAAAGAGGGCTT
Oi01 GACGTTTGCAGAAAGGCACGGTAATAGCAGGAGAAAGGGTATTTATTTGAAATTAGAGAGGAGGGGTACTTACAGGCAGGTTGCTTTGTACAGAAAGTAGCCCTTGAAAAATCCGGATGCGT
Oi02 GAGCAAGACCTACTCTATAAGACTAGCCCAAAATCTAAAGGAGAAAGAAAGGAAATTAACATGACAAAAAACAGTTATTAAGCACCAATTTCCGCGCAGACCAATGTAGGTAGCTTACTACGAC
Oi03 ACAAAGAAAGAAATGATCTAATTGAGAAATTAATTGCATCTAAATCAATTTTAAAAAGGGAACAAACATCTATATGAACCTGACAACAGCAGAGTTGGAAATACGAATACTTTAAATTACAATA
Oi04 CACTATGAATCTAAAAAGAGAGAGTGATAGGGGTAGATCAAGTTTCCCTTGATATCAAAAAAGGGAGAAATATATGGCATCTGTTGGATATAGCGGTGCAAGGTAAAAAGTAGCGCTTTTACGT
Oi05 TCTTTTATTGGCACTTTGAAATAGGATAGAAAGTTATAAGAGATCCCGTACCAACATATATCAAAAGGAGAGTTTAGCCCTTATGCGCTGCAAAATCGACGTTTATTTACTTCAGAGTCAGTAAC
Oi06 TAAAGAGGAGAAATAAGATATGATA TCCATCGAAGGGTTAAGTAAAGTATTTTCAATTAATAAANAAGACATCAAAAGCTGTAGACTATTGACCTCAATATTGAAAAATGGCGATATTTAT
Oi07 TAAAAAACACGCAATCTCTATTTTGTATCATTTGTTTAAACCACTAAACCAAAAAAGGAGATGCGTGCAATGCAATTTCTAACATAACAATTACCTGGGTTGGAAAGGAAAAATATA
Oi10 CTGGTTGCCGATTTTGGAGGGTGGTTGCGTAATGTAGAAGATGAACAGATGCTCTCTACTTTTGAAATATGCAAAACAGGTAA TTCAGCACGGGAGAAATGGGGAATATGATACGACTTT
Oi08 CTTCAAAATATGAGTAAACCAATCAGGTAACATAAGTAGGGGATCGAAACCTGTCAAGTGTATCGTAGTTTATAAAAAATCTAAAAATGAAGAGGAGCGGTGTATTTGCAAACTATAAAAAAC
Oi09 ACAGATGCTTAAATTTCAATCTTTGCAAGCAGAAACAATCTTACTTCAGGAGACAGGAACCAACCACTCAACTGTTTCACTGCTGCAAGTTCCAAATTTATCAAACTACGTCCTATGTGT
Oi10 CTGGTTGCCGATTTTGGAGGGTGGTTGCGTAAATGTAGAAGATGAACAGATGCTCTCTACTTTTGAATATGCAAAACAGGTAA TTCAGCACGGGAGAAATGGGGAATATGATACGACTTT
Oi11 TGTGACATTTGTCGGCAGCCCCCTCCGAACATACTAGATCTGAAAAAGTACTACATTTTAGGGAAATCAATTAAGTGAACAGAAATTCCTATGTGACCCCATATTTCTGTTAAAGATGTAC

Oi12 AAGACA TTCACACTAGGAAAAAAGTAAGAAAGTATCTCTAACGATCGAAAAAGGAGATATTTATGGATTTATTGGTTTCACGCGTGCAGGAAAAAGTACCTTGCTT
Oi13 **TC**TCCACATCGATTGTATAAAGGAGCTCCGGGTCAATTA TCGGATTGGCGCGGATGTCTTGGAGGAAATTCCTGTACTGCTTGAAGAACTGTCAGTTAATCGTATACAAAGTTATCGCAGGGA
Ca01 GAAATTTTGAGACAAAAGCAGTTTCATGGGAGAGTGGTTTGAGAGCAGAACTGGGGCAATAAGCTACCCAAATACCAAAGTTCTACCTTTAGACATGAAGGCTTAATAATAAGGAACCTG
Ca02 AAGAAATTTGTTAAATAACAAAATTTTAGTTTAGATGGTGTATGGGAACA TGTAATCAATCCCTTTAACTAGATGAAGGCGACTTTAAAGGTTCCCTTATACCTCAATCTATCTCTAAAAATATTTTACTA
Ca03 TTAAGAAGTGGGTATAGACATATTTTATTAAGAAGAGAGAGAAATACCTCCAAATATTTCTCCCTTCAAATCCCAATAAGCTTATAGATTTTACCAAATCTATCTCTAAAAATCAACTTACTTTAG
Ca04 AAATGTTTCTAAATATTTTTCAGGAAATAAGGTTCTTAAGAATGTTGATCTGAAGATTAAGGCGGAGAAATAATTTGGAAATGTTGTGTCATAGTGGAGCTGGAAAAAGTCAACAATTACTTTAG
Ca05 AAAATACCTGATAATCTTCCAGCAGCAAAAACCTTTAAATGAAGAAAAATATATTTTATGGAATGAGGATAGAGCCCTATCATCAAGATATAAGACCTCTTAATATTTGTTATAGTTAAACCTT
Ca06 AAGGGGATTTTAAAAA**ATG**AGTGAAGAAAAATTTGGTTTGAACATACAGGTTTCAGAGCAAGTTCTGTATCCAACTACAGGAATGGAAGAGTTGCTTGTGAAACTACAGTGAC
Ca07 ATCTGAAATCAGTAACAGAAAGGCAATCCAGATAAAAATCTCGGATCAAAATATCAGACGCTATTTTAGATGCCATATTTGAAAAAAGATCCAAATGGAAGAGTTGCTTGTGAAACTACAGTGAC
Cp01 TAAITTAAGCTTTAAAGATATATTTTGAATCGTGGGAAGATAAAATTAAGTTATTTGTTTAAATAAACAGGGTTGGAAATAAAATAAAATGAAGGGGTGAATTAGCTATCTTATATGATA
Cp02 GAGAA**ATG**AAAAAAGGAAAGTTTCAGCATATTTACCATAATTAATTTTGTATCGATTTATTTGGAACTTCAATTAGTAAATGAAGAATTTCTACTCTGTATCTGTATTTAGTTTCCAGGA
Lm01 TATTAGTAGCGGTTATCTCGGTTTTTGCCTTGGTTTAAACGGCTTCGGAGGTTTAGGAATGACGATGTTGGAGGAGGCTGACGATAAAGGCTTAAGCACAGAAAAA
Lm02 GAGGAAAAA**ACATG**AAAAAATTAACAAAAGGTTAGGAATTTTACTTGCCATCAAAAGCCTTTGTTTAGGAATGACGATGTTGGAGGAGGCTGACGATAAAGGCTTAAGCACAGAAAAA
Lm03 **TC**AGTAATCAGTATAAATTCGAAACAAATTCAGTACACGGCGGACACACACCGGACGGAGATACACATCTTAGAGCCGTACCTATTTATCAAAAGCAGCTATACACATTTGATAGGCTGCAAAATCGAAAAATA
Lm04 TAGCTCCAATTTATGCAGATCATGTGGGAAGTATTTTACGCACAAAAGGGAATTTAAAGACGCACGAGAGAAAATCCAAAGTGGCGAATAAACAGCCTTAGAGTTGCGCAAAATCGAAAAATA
Lm05 CTAAGAACCGTCACTATTTTACATCAGAAATCGGTTTCTGATGGACATCCAGATAAAAATTTGCAGATCAAAATTTGCAGATCAAAATTTCTGTGCAATTTAGATGCCAATTTATTCAAAAAGATCCCGACGCGCTG
Lm06 GATTAGTTCAAACTTTGGGTATCCGAGACTTGGGAGAAACGTGAAATGGAACACGTGCTGTAGAAAAATTTCTGGAAATGTTGGGATGTTGAGGTTATTCGGAGCTGTTAAAG
Lm07 AAACGTTGTAAGAAGATACACGTCCAGAAACAAACAAAGTTCTCGCAGTCGATCATGTGCAATTTAGAAATGGAACAAGGCGAGATTTTCGGAGTTGTTAGGTTATTCGGAGCTGTTAAAG
Li01 TTAGTAGCGGTTATCTCGGTTTTTGCCTTGGTTTAAACGGCTTGGGAGGCTTGGCGTAGTTTCAGACAAAGCAACACGTTTCAGGCAAAAGCGAAAAGACGGCGCTCTCTAAATTTATCGGT
Li02 GAGGAAAAAAG**ATG**AGAAAAATTAACAAAAAGGTTAGGAATTTTACTTGCAATCAAGCCTTATTTCTAGGTTAGCAGCATGTGGAGGCGGAAGTGACGATAAAGCCTTAAGCACAAAAAGAA
Li03 **TC**AGTAATGAGTATAAAATTCGAAACAAATTCAGGTACACGGCGGACATACACCGGACGGAGATACGCAATTTCTAGAGCGGTACCAAATTTATCAAAACACATCGTATACATTTGATAGCCCCAG
Li04 TGGCACCATTTTATGCAGATCATGTTGGAAGTATTTACGGACAAAGGCAATTAAGAGGCACCGAGAAATTCCAAAGTGCGGAAATTTCCAAAGTGTGCAATTTATTCAAAAAGATCCGGACGCGACGTG
Li05 CTAAAAACCGTCACTATTTTACATCGGAAATCGGTTCTGATGGACATCCAGATAAAAATTTGCAGATCAAAATTTCTGATGCAATTTTAGATGCAATTTATTCAAAAAGATTCGGGGAACAAAAAGCTCT
Li06 GATTAGTTCAAACTTTGGGTTATCCGAGACTTGGGAGAAAACGTGAAATGGAACACGTGCGCTAGAAAAAGTTTGGAAATGGTGGCAATTTTCAGAGAGGAATTAATTTGGCGGGAACAAAAAGCTCT
Li07 AACGTCGTAAAAAGAAATACGTCAGAAATAACAAAGTTCTCGCAGTCGACCATGTGCAATTTAGAAATTTGAACAAGTGAGATTTTCGGAGTAGTTGGTTATTCAGGGGCTGTTAAAAAGT
Sa01 TAAATCTAGGAAAATTTATACAGAAATCTGGGGAAGTCAATAGATAACTTTCGTTTGGAGATATGAGCATGTTGGTTATCATGGACAACCAATTAAGTTAGTTGTGTTGTCAATGCAATTAACCTGGCA
Sa02 AGAAGTTGTTAAAGAAATATCGGACTAAAAATAAAGAAAGTCTCGTGTAGATCACGTTAAATTTATCGAATTCGACGAGGATCGAATTTATGCGGTCAATCGTTTTTCTGGACGAGGAAAAAG
Sa03 GCAA**ACTATG**TAAATAACAAACGATTAATTTACTTTCAGAGTCTGTTACAGAAAGGACACCCAGATAAAATCGCTGACCAAGTGCAGATGCAATAATAGATGCTATTTTAAAAAGACGACCC
Sa04 ATGCTTGGGCAATATCCCTTGTATTATTTGTGGCGTTGTTTTAGCGGTAGGTAATTAACAGGTGATTTTACTTCAATGCCAATTAATGTTTGCATTAACGATAACCGTAAATTTGTGG
Sa01 AGTGGCGCCACAGGGTTCCGCTCGGACCGGCTTCGCTCGGAAGAGTGTTCGGCCCCCTCGAGATCGCCTACGACTCTTCGGACTACGCCGAAGACTCGGCAACGGGATCGGAAG

Cons

[illegible]

Ba14 TCAAAAGGAAATTGTAATAGGTGATGGTGGGTTGGAAACATTATTACATTCACACGGTTTGC AAAAGTAGITTTGAAGAAATTGAATATATCTGATCCAGATTTAATTATATCGATTTCATAAG
Ba15 AATTAAAGGATGAGTTCCGTACAAATATATACAAATTACTGTAGGGAGGTTTACCACATGACAAAAAACGTCATCTGTTCACATCTGAGTCTGTAACTGAAGGACATCCAGATAAAAATTTGT
Ba16 ACGGTGGCTACCGTATCAAAAAATAAAAAATTGCGGAGTCAATCAAAAAATTAGTCCAGCGGTAGAACAGTCGGTCTTTCATCCCTCCCTATGAGGCCAAAAAGCGCCTCTAAAGTCTG
Ba17 GGAAAGGAACGATTTGTGTCAAGGTGGCTATACGCCAAAAGAAATGGAGAACCGCGTGTTTTACCGCTTTATCAAAAGCACGAGTATAAATATGATACTTCCGATGATTTAGCAGCATTAAT
Bc01 GGGAAAAAATGATTTCTTTTAAACAAATGTAAGTAAGTATATGAACACAGGTGGCAATCTGTTCATCGGTGGAGGATGTAAACATTATCAAGTTGAGAAAGGCGGAAAAATTTTGGCATTTATCG
Bc02 TGGTTGCCGATTTTGGGGATGGCTTCGGAAATGTAATGTAATCTATGCCGCTACGTTTGAGTATGCAAAACAAACGCGCAAGCGGCAGAACAAATTAGGTTTTTCAACAACACITTT
Bc03 TTTGAGGAAGTATCTGAGAAAAATTGAAGCGATGCTTCCTGATATGAATATGGTTCAATTACAAATTGTTGTGCAAGATGGCAAAAGTCATTCAATTAGAGAAAAAGTGAAAAAGTACGTTTA
Bc04 AAGAAACGAGAGGAAATGGTTGGCATTATTACCACITTTGGGATATTTTGGCGCTATTTATTTGGTTCTGGAAATTTATACAGGTGATTTCTATAAATTGCCGATACTTTAGCAATTTTCAA
Bc05 AATATAGAGTAAATAAAGTTGACTATTAAAGAGGGGAGAAATTGTAATGAATAAATTATCAACAAAAATTAGTAGTGGCAATCGGAAATGGAGCAGCATTAACGGGATATTAGGACTTTGGG
Bc06 CGTCACAAAAGAAAAACAATTGAAGAGAGTATTGAAAGAAATAAGGAAAAAGTACATAGAAAAAGTACATAAGAAACAAAGTCACGATATTCAATCGGAATCCGGAGATTGGTAACCAAGAGTTTACGCATCAAGAA
Bc07 TAGAAAGTTTCCGCAATTATTAAAGTATGTATACATAACITTAGGAAATTACTGTAGTTTCAATGATTATTTCTTTTGTATAGGGATAGGTTTGGCGATCATAAACGAAAAACAAAAACGA
Bc08 GGTTGCCGATTACTGTGACACTCGAAAAATACGTCAAACTGCCGTAGTACAGTTTATGAATATATGATAGCAAGATAGGCCAATAAGCCAAATATCATTTGTAGATATTCAAAGAACATATCGTTTCGC
Bc09 ATTTAATCCATGATGATTCACATAACTTAGAAAAAAAAGCTGAGCAAAATGGCACTCGGTTTAACAAATTGGCTTTGGACTCATTTGCCACATTTTGCCACATTTTGAAGAACAAATTAAAGCAGCATAT
Bc10 TCAAAAGGAAATTGTAATAGGTGATGGTGGGTTGGGACGTTTACATTCACATGGTTTACAAAGTAGTTTGAAGAAATTGAATAATACTGTATCCAGATTTTAAATTATATCGATTCATAAG
Bc11 ACATGTCAACTATCGAAACAAAAATTAGCGCAAAATCGGAAACCGGAGTGAAACTACAGGAACGTGTAATCCACCTGTTATTTTCACTGTTATTCGTCACGAAGGAAATGGTAAAT
Bc12 GGGATATTATGCATTAACTGAAACACAGCTATACAATATCGGAAAGAACACCGGTTATTTGAAAAAGAAAGCAAAATGTATTTTGTCTAGAAATGGAGATGGAAATTTAAATTACGTGT
Bc13 AATTAAAGGATGAGTTCCGTACAATATATACAAATTACTGTAGGGAGGTTTACCACATGACAAAAAAACGTCATCTGTTTCACATCTGAGTCTGTAACTGAAGGACATCCAGATAAAAAATTTGT
Bc14 ACGGTGGACTACACGCATTAAACATAAAAAAATGCGGAGTCGATCCAAACAAAAAGGGGTGATACACCATGATTTCTATTAGAGAAATGTAAAGAAAAATATATAAGCAAAAAAGCGGTGAT
Bc15 GGAAAGGAACAAATTTGCGTGCAAGGTGGCTATACGCCAAAGAAATGGTGAACCGCGTGTTTTACCGCTTTATCAAAGTACAAACGTATAAATACGATACTTCCGATGATTTAGCAGCCTTAT
Bc16 GAAAAATCAATGAAAAAAAAGTTTGTACCCGGTATTGCATCAGTTGTAGGAGTAAGTATTTTATTAACCTGGTTGCGGTAGTTATAAAAAACGAAGCAAGCGGAGCAAAATGCAAAAAGACGAG
Bc17 TATTAAAGCATTGTAAGTGGGCTGTATTATTAAAGCGCATGTAGCGGAGTTTCAGATAAAGAAAGTAAAAAGCGTTAGATGAGAAAAAGATTACTGTCCGTGTAAACAGGAGGGCCTCATG
Bc18 AAACTAAGTAAATATATGTGTTTAGGGGTTATTGGAGTGTATGTAATTAATAAATATACAGTTATGGGTGTTACGCTATGGGTTATTACGACCGGTGACATTTCTTAATTATGCCATATTAT

B. Cobalamin Riboswitch Alignment.

ID	Start	End	Accession	Organism
Atu01 +	70441	70625	NC_003304.1	Agrobacterium tumefaciens
Atu02 -	441331	441136	NC_003305.1	Agrobacterium tumefaciens
Atu03 +	877645	877833	NC_003304.1	Agrobacterium tumefaciens
Atu04 +	921717	921886	NC_003305.1	Agrobacterium tumefaciens
Atu05 -	1640563	1640420	NC_003304.1	Agrobacterium tumefaciens
Atu06 -	2810076	2809899	NC_003304.1	Agrobacterium tumefaciens
Bha01 -	466904	466746	NC_002570.1	Bacillus halodurans
Bha02 +	528894	529051	NC_002570.1	Bacillus halodurans
Bha03 +	870599	870748	NC_002570.1	Bacillus halodurans
Bha04 +	1661078	1661219	NC_002570.1	Bacillus halodurans
Bsu01 -	3403719	3403620	NC_000964.1	Bacillus subtilis
Bja01 +	2232813	2232975	NC_004463.1	Bradyrhizobium japonicum
Bja02 +	3617311	3617490	NC_004463.1	Bradyrhizobium japonicum
Bja03 +	3630677	3630857	NC_004463.1	Bradyrhizobium japonicum
Bja04 +	3634122	3634284	NC_004463.1	Bradyrhizobium japonicum
Bja05 -	5279669	5279495	NC_004463.1	Bradyrhizobium japonicum
Bme01 +	679030	679218	NC_003317.1	Brucella melitensis chromosome I
Bme02 +	717388	717585	NC_003317.1	Brucella melitensis chromosome I

Bme03 + 559758 559950 NC_003318.1 *Brucella melitensis* chromosome II
Bme04 - 973106 972933 NC_003318.1 *Brucella melitensis* chromosome II
Ccr01 + 502968 503156 NC_002696.2 *Caulobacter crescentus*
Ccr02 + 1925017 1925166 NC_002696.2 *Caulobacter crescentus*
Cte01 - 409802 409630 NC_002932.3 *Chlorobium tepidum*
Cte02 + 422045 422244 NC_002932.3 *Chlorobium tepidum*
Cte03 + 443769 443951 NC_002932.3 *Chlorobium tepidum*
Cte04 + 584183 584411 NC_002932.3 *Chlorobium tepidum*
Cte05 + 882576 882770 NC_002932.3 *Chlorobium tepidum*
Cac01 + 1509969 1510116 NC_003030.1 *Clostridium acetobutylicum*
Cac02 + 2557903 2558041 NC_003030.1 *Clostridium acetobutylicum*
Cpe01 + 248269 248429 NC_003366.1 *Clostridium perfringens*
Cpe02 + 1241749 1241887 NC_003366.1 *Clostridium perfringens*
Cpe03 - 1431291 1431152 NC_003366.1 *Clostridium perfringens*
Cpe04 - 1549481 1549348 NC_003366.1 *Clostridium perfringens*
Eco01 + 4160983 4161133 NC_000913.1 *Escherichia coli*
Fnu01 + 934517 934658 NC_003454.1 *Fusobacterium nucleatum*
Lig01 + 1347854 1347994 NC_004342.1 *Leptospira interrogans* chromosome I
Lmo01 + 1179829 1179979 NC_003210.1 *Listeria monocytogenes*
Mlo01 - 1101076 1100918 NC_002678.1 *Mesorhizobium loti*

Mlo02	+	1149143	1149308	NC_002678.1	Mesorhizobium loti
Mlo03	-	4044577	4044416	NC_002678.1	Mesorhizobium loti
Mlo04	-	4957334	4957164	NC_002678.1	Mesorhizobium loti
Mlo05	-	6170855	6170715	NC_002678.1	Mesorhizobium loti
Mlo06	+	6749148	6749315	NC_002678.1	Mesorhizobium loti
Mle01	-	1130394	1130222	NC_002677.1	Mycobacterium leprae
Mtu01	-	309822	309703	NC_000962.1	Mycobacterium tuberculosis
Mtu02	-	1261701	1261497	NC_000962.1	Mycobacterium tuberculosis
Pae01	+	1381520	1381688	NC_002516.1	Pseudomonas aeruginosa
Pae02	-	3261415	3261204	NC_002516.1	Pseudomonas aeruginosa
Pae03	+	3265563	3265728	NC_002516.1	Pseudomonas aeruginosa

ID	Start	End	Accession	Organism
Pae04	-	3305780	3305629	NC_002516.1 <i>Pseudomonas aeruginosa</i>
Ppu01	-	2765203	2765045	NC_002947.3 <i>Pseudomonas putida</i>
Ppu02	-	2768953	2768785	NC_002947.3 <i>Pseudomonas putida</i>
Ppu03	+	3857563	3857746	NC_002947.3 <i>Pseudomonas putida</i>
Ppu04	-	3981958	3981816	NC_002947.3 <i>Pseudomonas putida</i>
Rso01	-	2609233	2609017	NC_003295.1 <i>Ralstonia solanacearum</i>
Sme01	+	954780	954943	NC_003047.1 <i>Sinorhizobium meliloti</i>
Sme02	-	1999747	1999574	NC_003047.1 <i>Sinorhizobium meliloti</i>
Sme03	-	2122891	2122516	NC_003047.1 <i>Sinorhizobium meliloti</i>
Sme04	+	66265	66456	NC_003078.1 <i>Sinorhizobium meliloti</i> plasmid pSymB
Sme05	+	580403	580578	NC_003078.1 <i>Sinorhizobium meliloti</i> plasmid pSymB
Sco01	+	1037869	1038053	NC_003888.1 <i>Streptomyces coelicolor</i>
Sco02	+	1045899	1046106	NC_003888.1 <i>Streptomyces coelicolor</i>
Sco03	+	1051420	1051563	NC_003888.1 <i>Streptomyces coelicolor</i>
Sco04	-	5688395	5688291	NC_003888.1 <i>Streptomyces coelicolor</i>
Sco05	-	6532337	6532191	NC_003888.1 <i>Streptomyces coelicolor</i>
Sfi01	+	4183416	4183566	NC_004337.1 <i>Shigella flexneri</i> (*)
Son01	+	826836	827026	NC_004347.1 <i>Shewanella oneidensis</i>

Son02 + 1071692 1071874 NC_004347.1 *Shewanella oneidensis*
 Sti01 - 2114053 2113918 NC_003197.1 *Salmonella typhimurium*
 Sti02 + 4347871 4348024 NC_003197.1 *Salmonella typhimurium*
 Tma01 - 84288 84144 NC_000853.1 *Thermotoga maritima*
 Tte01 + 395153 395353 NC_003869.1 *Thermoanaerobacter tengcongensis*
 Tte02 + 396075 396275 NC_003869.1 *Thermoanaerobacter tengcongensis* (*)
 Vch01 + 145142 145306 NC_002505.1 *Vibrio cholerae* chromosome I
 Vvu01 + 1165724 1165882 NC_004459.1 *Vibrio vulnificus* chromosome I
 Xac01 - 3631166 3630987 NC_003902.1 *Xanthomonas campestris*
 Xax01 - 3758428 3758245 NC_003919.1 *Xanthomonas citri*
 Ype01 - 4393235 4393008 NC_003143.1 *Yersinia pestis*
 Aca01 - 340 170 M34485.1 *Acinetobacter calcoaceticus*
 Avi01 - 388 214 U45329.1 *Agrobacterium vitis*
 Bfr01 + 580 762 AY043208.1 *Bacteroides fragilis*
 Bmg01 + 1211 1350 AJ000758.1 *Bacillus megaterium*
 Lma01 - 76392 76234 AL499620.1 *Leishmania major*
 Pfr01 - 543 373 AY033236.1 *Propionibacterium freudenreichii*
 Rca01 + 105327 105521 AF010496.1 *Rhodobacter capsulatus*
 Rca02 + 116991 117174 AF010496.1 *Rhodobacter capsulatus*
 Rca03 - 39849 39672 AF010496.1 *Rhodobacter capsulatus*

Rsp01 +	201	341	B07728.1	Rhodobacter sphaeroides
Sbi01 -	330	147	BH245584.1	Sorghum bicolor
Sgi01 -	9209	9035	AF263012.1	Streptomyces griseus
Svi01 -	1235	1052	U27616.3	Stealth virus 1
Zmo01 -	24942	24808	AF193754.1	Zymomonas mobilis
Zmo02 -	4323	4162	AF193754.1	Zymomonas mobilis

Accession numbers are for Genbank sequence entries. Start and end positions are the 5' and 3' nucleotides of the first interior UG base pair of stem P1 (orange). Secondary structure (SS) and sequence consensus (Cons) lines are shown above the alignment. In the consensus sequence, uppercase and lowercase letters represent $\geq 90\%$ and $\geq 80\%$ conservation at a position, respectively. The degenerate bases R (A,G) and Y (C,U) appear only when a single base is not 80% conserved. Sequences marked with an asterisk (*) were excluded when determining the sequence consensus because they have $>90\%$ identity to another sequence in the alignment.

SS	<<<<<<	GGU y	r AA GGGAA yGGUr	1A
Cons				
Alu01	UACUAUAUGUGGUGUUAAGGUU-CUUC	CGUA	GGGUUGGGAGCU--AAAGGGGAU	UCCGUUCCGUAAACGCC--AUCAC--GGCGGAGCAAGG
Alu02	CCUUAUGUGAGAAACGACGGU--UCCUACAGCC	GAAA	GGCGAAGGGAUU--AAUA	GGGAACAGUGGUGCGGCGA--UCUUUU--UCGUCCAAUG
Alu03	CGGAUACAUGUCCUGAUGGUU-CCUUCGGG	CGU	UCCGGAAGGUG--AAAGGGGAAC	ACGAUAGGGA--CAAA--UCCUCAU
Alu04	GACAUUGGUUAGCCAUUGGUU-CUGCGGAC	GAA	GUCGGAAGCU--AAAGGGGAU	UCCGUGAGGGGU--UUAAUCAC--AGCCUGAAU
Alu05	CCCAUAGCUUCCCGGUCAGGUG-CCCGC	CUUGC	GGCGGAG--AAUGGGGAU	CCCGUGA--AAGA
Alu06	CUAAGGUUAGGACUGACGGU--CUUUUCCCG	GCAA	CGGAAAAGCU--AAAGGGGAAC	ACGGUUCGCGCC--CGAGAAA--GGGUCAUU
Bha01	AUUUCAUGUUGGGAACAGGU--ACGUUAGUC	ACAUGUA	GACUUAUUGUU--AAAGGGGAU	CCCGUGC--AAAU
Bha02	UAGUGUUUGGACGGUAGGU--GCC	CGAAGC	GGCUU--AAAGGGGAU	CUUGUGC--AAAU
Bha03	UAAACACGCUAAGCAUUGGU--GGUCAA	ACAUCGG	UUGAAUCUG--AAAGGGGAAC	CUUGUGA--AAAU
Bha04	AUCGUUAUUCGCGCUGAAGGU--CGUCAA	UGU	UUGAGCGUG--AAAGGGGAAC	UCCGUGA--AAAU
Bsu01	CGGAUACGAUUGUCAAUAGGU--GCCGGUCCGU	GAACA	ACAGCGGCUU--AAAGGGGAU	CCCGUA--AAAG
Bja01	CGAUAAUCCAAGUGUGGAGGUU-CUCCGUUC	CCAUU	GAUCCGAGGU--AAGA	GGGAACCGGUGC--AAUG
Bja02	CAAUUGUGCCCGCGGUUGGU-CCUGUC	CUAU	GACAGCG--AAAGGGGAU	CCCGUA--GGCGGACCC-AGUUGC--GGCGCCCAAA
Bja03	GGGCACAGGACGGGCAUGGU--GCUGAGGUGCGC	AAA	GGCGCGGAGCAU--AAUGGGGAU	CCCGUGC--UGUU--UCCCAUUG
Bja04	AAUCCUAGAUUCUGGACCGGU-UCCGCC	GAGA	GGGAUG--AAAGGGGAU	CCCGUGC--UGUU--UCCCAUUG
Bja05	UCGUAGAUUGGUGGUGACGGU--UCUCC	GCAC	GGGAUC--AAAGGGGAAC	GUUGUGGAGAUUGUCCCAUUGCCGGAUUGUCCCAACG
Bme01	AUCGCAAUUUUCAGGACAGGU--UUGCCCG	AUUGC	GGCGAUG--AAAGGGGAAC	ACCGUGAAGCC--AUAG--GGCUGAAA
Bme02	AGUGUCAAACAUUGACAGGU--UUGCCCG	AACGAUCC	CCGGCAUACC--AAAGGGGAU	CCCGACGACGCC-ACGCC--GGCGGUCUUUA
Bme03	GCCGUAAUACCGUACUAGCGGU--UCCCGACCG	AGAG	CGAAGGGGAU--AAUA	GGGAACACGGUGAGGACGACCG--AUCAA--GGGGCCGAGA
Bme04	UACCAUAUCUUGUUGGAGGUU-CUUUCGAUUC	GAC	GAGUCCGGAGCU--AAAGGGGAU	CCCGUGGCGUUGGCC--AUGGU--GGCGGGGCAUUG
Ccr01	GGUCUUGCCGUUGUGGUGU-CUGCGGACG	UUCG	CGUCCGAGCU--AAAGGGGAAC	UCCGUG-AGGG--CGUGAAA--CCCUGAAU
Ccr02	UAGCUCUAGCUUGGUGUAGGU--UCCUC	GAAA	GAGGAUG--AAAGGGGAAC	GAGGUG--AAGA
Cte01	AUACUUAUCCGAUUAUGGU--GCCCGCCAUG	GAAA	CAUACGGGCUU--AAAGGGGAU	CCCGUGA--GAGU
Cte02	GUUCUUCUGGCAUGACAGGUG-CCGGUU	UAAA	AGCGGAG--AAUA	GGGAACUCCGUGA--GAUU
Cte03	CAUAUAAUAAUUCAGUUAACGU--UUCCGGUGCC	GGUG	GGCGCGCGGAUUG--AAAGGGGAAC	CCCGUGA--AAAU
Cte04	UGAGUUCUUAACGAUUAACGGUG-CCGGAU	GAAAG	AUGCCGAU--AAUA	GGGAACUCCGUGU--GAUU
Cte05	GUUCUUCUGGCAUGACAGGUG-CCGGUU	UAAA	AGCGGAG--AAUA	GGGAACUCCGUGA--GAUU

Cac01 AUUGCUACUAAAUAUUGUAGGU--UCAACUGAG--GAGU-----CUUAGUUGAUU--AAA**AAGGAAU****U****CAGGUGA**-----AAAG
 Cac02 GAAUAAUACCAUAUUUUAGGC--ACCUA-----UAGGUUU--AAU**A****CGGAAAU****UUGGUGA**-----AAAU
 Cpe01 AAUUAAAAUAUUUAGAAUAAGGU--UAAAUAGUUAC--AUUU-----GUAACUAUAUAUU--AAA**CGGAAU****UUGGGUUU**-----AAAU
 Cpe02 AGUUGAUUAACUAAUAUUUGGU--GUG-----AUUU-----CCUU--AAU**CGGAAU****U****GAAGUUA**-----AAGU
 Cpe03 AUAAUAUUUUUAUUUUUAGGU--UUG-----AUUU-----UAAUU--AAA**A****CGGAAAU****GUGGUUA**-----AAGU
 Cpe04 AAAUAAAAUAAGAGCAUUAGGU--GUU-----UAGU-----AACUU--AAU**A****CGGAAAU****GUU**-----AAA-
 Eco01 CCUGUAGCAUCCACUUUGCCGUC-CU-----GUG-----AGUU--AAU**CGGAAU****U****CCAGUUC**-----GAUU
 Fru01 UUUUAUAUCAGUCAUUUAUUU--CCUUA-----UUUU-----UAAGGCU--AA**A****CGGAAU****U****UUGUGA**-----GAUA
 Lig01 AUCUUGGAAACGGAAACUUGUUU-AUU-----CUCGU-----GAUGA--GG**A****CGGAAU****U****CCGUUUC**-----AAAU
 Lmo01 GUUAAAUAGGUCUUAUUGUGU--GGAUUGU-----AUGU-----ACAUUUCUG-AAA**C****AGGAAU****U****UCGGUUC**-----GAUG
 Mlo01 CUUAUGUCAUGCAGUCGUCGU--UCC-----GUUUU-----GAGGCC-AA**A****CGGAAU****U****CCGGUCCGGCGA**-----AAUUC--UUGCCCAAUG
 Mlo02 GCCUAAAUCCGCUCCAGACGGU--CCCUUGCC-----CGCAAC-----GGCAGGGGCU-AA**A****CGGAAU****U****CCGGUCCGGGUA**-----UUCG--AUCUCAAAU
 Mlo03 AUUAGAUAUGUCAUCUGAGGU--CCGUUCGU-----GACG-----ACGGGGCGGAG--AAU**U****CGGAAU****U****CCGGUCCGGU**-----AAGU
 Mlo04 GUGAUUUGCGCAUGUCGUGGUU-CUCCGCGCGG--ACU-----GCCGUAAGCGGAGCU--AA**A****CGGAAU****U****CCGGUCCGGU**-----GAUG
 Mlo05 AAGGUCGCCGCCACUGCCUGGUG-CCCGC-----CCCA-----GCGGGAG--AAU**C****CGGAAU****U****ACGGUUG**-----AAU
 Mlo06 UCUACGGUGGGUGCGUAUGGU--CCCGCGCGC-----GAAA-----GGCAAAGGGUG--AAA**A****CGGAAU****U****ACGGUUGAGACCU**-----CAA--AGGUCGAGA
 Mle01 CCACACGGCGCCAGUAUCGAGU--GAUGCU-----AGCUC-----AGCAUCGC--GAG**A****CGGAAU****U****CCGGUGA**-----GAUU
 Mlu01 CUUCCGUCAGGCCAUGACGAU-----G**CGAGGAAU****U****CCGGUGA**-----GAUU
 Mlu02 -----UUGACCAAGCAGCUGGUC-UUCUGGCGUCCGAAAGGGCGUCGCAUCGA**CGCGGGCA**ACGA**UCCUUCGC**-----GAG**A****CGGAAU****U****CUGGUGA**-----GAU
 Pae01 AGCUGCGCGCCUUGCGACAGGUUG-CCCC-----GCAA-----GGGUG--AAA**C****CGGAAU****U****CUGGUGCGUUCG**-----GUC--GGAACCAGG
 Pae02 GCAUAAUAGCGGUUCGUUCGU--GCCCGGCCCUUUCGCG--UUAG--CGCGGGCCCAACGAGGGCCG--AA**A****CGGAAU****U****ACCGA****CGCGCGGUCU**-----UUCG--AAGCCCGGGCCUAG
 Pae03 UCCCAUCCGGGCCGUUCCAAGGUG-CCUCCUGC-----CGCCGC-----GCAGGAGGUG--AA**A****CGGAAU****U****CCGGUCCGUCAC**-----UUCG--GUGAUCAGU

Pae04 CGUAGCCUUGCCGGUUCGAGGUU-CCUCGCCG-----GCGA-----CGCGGGGCU--AAC**A**GGGAAC**U**CCGGUCC-----AUG
 Ppu01 GUCUACCAUGCGGCCGCCGGU--UUCC-----ACCAC-----GGAAU**U**CC**A**-----GGCCUG-----CCAAUA-----CAGGCC--AA
 Ppu02 CAGAUCCGCCAGUUUCAGGUG-CCCUGCC-----CGCCGC-----GGCA**U**CCGGAA**U**CCGGUUGCGUGUG-----UUGCC-----CACGACAAGU
 Ppu03 UCCUUAUGCCUUCGGUUCAGGUG-CCCG-----UCAG-----GGGUG--AAAC**U**CCGGAA**U**CCGGUUGCGUCCAGGCCUUCAGC-AGGGCCGGACAAGU
 Ppu04 CGUAGCCUUGCCACUUCGAGGUU-CUUCGCC-----CUG-----GCCGAA**U**CCGGAA**U**CCGGUCC-----AAG
 Rso01 GUUACACUGCCGGGUCUGGUGCCGAG------GCCGA-----UCUGCAGUU--AAAC**U**CCGGAA**U**CCGGGAGCGGGCCGC-----CCAAAC-----GGUGCGCCAA
 Sme01 CUUAGAUGAGCACUCUAAAGGUG-CCGCCUC-----GAAG-----GGAGGCGGAG-AAU**U**CCGGAA**U**CCGGUCC-----AAUC
 Sme02 UGGCCAUUUGCCGCCGUCAGGUG-CCCGC-----GAAAU-----GCCGGG--AAU**U**CCGGAA**U**CCGGUCC-----AGUU
 Sme03 UAAUUAACGCAUUGGAUGGU-UCUCUCGUGCC-----GAGGU-----GGGCGAGGAGU--AAAU**U**CCGGAA**U**CCGGGAGCGGCGACCC--ACGCC-----GGGCGCCCUUA
 Sme04 CACAUUAACUGGGACCGACGGU--UCCCCUACCC-----GUGA-----GGUGAGGGGAUU--AAU**U**CCGGAA**U**CCGGUUGCGGACGACCC--AAGA-----GGGACCAAAA
 Sme05 GCAUACCAGAUCAUGUGAUGGU--UCCGCC-----CGACUGAAGAAC-----GCCA-----GGCGGAUGCGUCCAA**U**CCGGAA**U**CCGGUCC-----GAAU
 Sco01 UAGGCGGCCGUGCAGCUGGU-CGCCCGUCC-----GCCA-----GGCGGAUGCGUCCAA**U**CCGGAA**U**CCGGUCC-----GAAU
 Sco02 UACGCUAGUCCCGCAGUUGGU-UCGGCCUCCUUGUC-----GAUCA-----GGUCUGCGCGCGGACGC-AA**A**UCCGGAA**U**CCGGUCC-----GAAU
 Sco03 GCAGACCGUAGUACAGCGGU--CAUCG-----CCG-----CGACGGG--AGA**U**CCGGAA**U**CCGGUCC-----GAAU
 Sco04 UAUUCUAGUCUGCGUUGCC-----GCCA**U**CCGGAA**U**CCGGUCC-----GAAU
 Sco05 ACUACUGUCCCGCAGCGUUGU-----GAU**U**CCGGAA**U**CCGGUCC-----GAUG
 Sfl01 CCUGUAGCAUCCACUUGCGGUC-CU-----GUG-----AGUU--AAU**U**CCGGAA**U**CCAGUCC-----GAAU
 Son01 UUUUGAGUCAACCUUCUGUGUG-CUUGCGAUG-----AUAG-----CGUCGCGAGAU--AAU**U**CCGGAA**U**CCAGUGA-----AAUU
 Son02 ACCUAGCUAUUGCAUUAAGGUC-AUAAACGCCGA-----UCAACCAAAU**U**-----AAU**U**CCGGAA**U**CCGGGCGCUG-----CCCGU-----CAGCCAG
 Slt01 GCCAUAAAGUAAACCAACAGGUUUGCCAC-----AUUU-----GUGU-----A**U**CCGGAA**U**CCAGUGA-----AAAU
 Slt02 ACGGUAGCAUCCGUGGCCGUG-CU-----GUG-----AGUU--AAU**U**CCGGAA**U**CCAGUGA-----AAAU
 Tma01 GAAGCCUCCUCCACCGUGCGGU--ACCC-----UUCG-----GGUUC--AAAC**U**CCGGAA**U**CCGGUGA-----AAAU
 Tlc01 UUGAAU**U**UAAAGCCUUAUGGU--CCC-----AUGAU-----GGUU--AAAU**U**CCGGAA**U**CCGGUGA-----GAAU
 Tle02 UGAUUAU**U**AAAGCCUUAUGGU--CCC-----GUGAU-----GGUU--AAAU**U**CCGGAA**U**CCGGUGA-----GAAU
 Vch01 AUACUACAGCGCCAAAGCUGGU--GCUAUUUAAGUCC-----UGGAU-----GGCUAA**U**UUGGUG--AAAU**U**CCGGAA**U**CCGGUGU-----AACU
 Vnu01 AUAGAUUGCCUCAAAGCUGGU--GCUAUCUG-----GAAGUA-----UAGUUGGUG--AAAU**U**CCGGAA**U**CCGGUGU-----GAAU
 Xac01 CUACCAUGCGCGGCCUGAGGUG-ACUGCCGG-----AAUU-----CCGUGGUUU--AAAC**U**CCGGAA**U**CCGGUUGCGCGCAUCCG--CUUG--GCCAGACGCAAGU
 Xax01 CUACCAUGCGCGGCCUGAGGUG-ACUGCCGG-----UUGG-----CCGUGGUUU--AAAC**U**CCGGAA**U**CCGGUUGCGCGCAUCCG--CUUG--GCCAGCGCAAUU
 Ype01 UACUUGAGUAGCAUUGUGGUGCCGCCUCAUGGUU-----AUUUA-----AACACCUAAAGUU--AAAU**U**CCGGAA**U**CCGGUGU-----AAAU
 Ace01 CUUUACCAUUCGUAA**U**CAAGUUA**U**AAAGC-----AUUC-----GCUU**U**-----A**U**CCGGAA**U**CCGGUGC-----AAAU

Avi01 CCUAAAGUGGAGCGUAUGGGU-UCUGCAAGUGU-----CAAA-----ACGCNCGCGAUG--AAA-**GGGAAU**-**ACCG**UGAGGACGACCC--AAGUAA-----GGGCCGAAA
 Bfr01 UUAUCUUUGCUCGCCUGAU^{CGGU}--UCCGAUAG-----UCAUUCU-----CUAUCGGAUU--AAA**A**-**GGGAAU**-**U**-**CGGGUGU**-----AAAA
 Bmg01 AUCAAACAGCAACAGUAAAGGU--GCC-----AAGAA-----GGCUU--AAU**A**-**GGGAAU**-**U**-**CGGGUGA**-----AAGA
 Lma01 -----UCGGGUG-CCCU-----UCAC-----AGGGUG--AA**A**-**GGGAAU**-**CGCGUGAG**UCAUGUUCUUAUCUCAAAGGCGUGACGAGU
 Pfr01 UGUGUAGGCUAGUAGUGCUGGUU-CGGCUGGC-----CCAC-----GGCAGUCGUCGCAAG**A**-**GGGAAU**-**U**-**CGCGUGU**-----AAUU
 Rca01 GCCACUCAGGCGCGGCGUGGUU-UCUGUC-----CUAU-----GACAGGCG--AA**A**-**GGGAAU**-**U**-**GU**GAAGGGAUUGCGACGGCUUU--GCCCGGAAACCCGA
 Rca02 GGCUACUCCAAACAGGCGAUGGU-UCCC-----AACUGGAC-----GGGAUU--AAU**A**-**CGGAAU**-**ACCG**UGAGGAUUACCC--AUCA-----GGGGCCUAAU
 Rca03 GGGCACCUUCGCGGCAGAU^{GGGU}-CCCGGCCAAGC-----CAC-----GGCGCGCGCGUG--AAA**A**-**GGGAAU**-**U**-**ACCGUGUG**GGUGUAGGC--AUCA-----GCCGCCAAAU
 Rsp01 UGUUUUGGCAAGGGGUCAGGNG-CCGC-----UUCG-----GGCGGAG--AAU**A**-**GGGAAU**-**U**-**CGCGUGG**-----AAAU
 Sbr01 UAGACUGGCCCAACUUCAGGUG-ACCUGGGC-----CAUG-----GCCGGCAGGUUG--AA**A**-**CG**-AA**A**-**CGCG**UGACGGUG-----AUUC-----CACGCCAGG
 Sgr01 UAGGCUGACGGUGCAGCU^{GGUU}-CGCCUUGUC-----GCCA-----GGCAGGUGUGCGCAAG**A**-**GGGAAU**-**U**-**CGCGUGG**-----AAAU
 Svi01 AUCGCUUCUUCAGGA^{AAGCGU}--UCUGCC-----GAGA-----GGGUGGAUG--AAA**A**-**GGGAAU**-**U**-**ACCGUGA**AGCA-----UUAAAAU-----UGCUGAUG
 Zmo01 CGGAAAUUUUUUGCAUAGGGU--UUCCUUC-----GAGU-----GAAAGGA^A--AAU**A**-**GGGAAU**-**U**-**ACCGUGC**-----AAAA
 Zmo02 AGCAUAGGAAGGAUUAAGGUU-CUUUGU-----CAUUG-----GCAAAAGCU--AA**A**-**GGGAAU**-**U**-**CGGUGCGAAA**-----GAUU-----UUUCAAAAG

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SS >>>>>> <<<< >>>> <<<<<<<<

Cons CCr RC Gy CCCGC RC GURa R

Atu01 CCGAAACUGCCCGCCGAAACUGUGA-CCGG-----CGAGCAUCGUCCGAUUUG-----
Atu02 CUGUGGCUUGCCCGCCGAAACUGUAA-CCGGAUU-----GUUGUUAUCCCGAGUGACGCUIUGAAGGGGUCAU-----
Atu03 UCGUGGCGUGCCCGCCGAAACUGUGA-CCGG-----AGAGCCUGAAACGAAAUCCACUGGCAA-----
Atu04 CCGAAACUGCCCGCCGAAACUGUAA-CCG-----ACGAGCGAAAGUCCAUCAU-----
Atu05 CCGGAACGUG-CCCAACGUGUAA-GGC-----GGAUGCUCUUUUCUCAU-----
Atu06 CCGUGGCUUGCCCGCCGAAACUGUAA-CCGGU-----AAGCCCGCACCGUAAA-----
Bha01 CCGGAACGUGUCCCGCCGAAACUGUAA-CCGG-----UGAGUUUGAACGUAUU-----
Bha02 CCGGAACGUGUCCCGCCGAAACUGUGA-CCGG-----ACGAACGGGAACGAUUU-----
Bha03 CCGGAACGUGUCCCGCCGAAACUGUAA-CCGG-----AGCUACAUGUGAGGAA-----
Bha04 CCGGAACGUGUCCCGCCGAAACUGUAA-CCGG-----GGAGAGGCUUGGAAGA-----
Bsu01 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----CGAGCCGUGUCCGACGAU-----
Bja01 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----AGAUGCCCGAG-----
Bja02 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----GAGGGGCUCCGAACC-----
Bja03 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----AUAUCCUUCGUCAGAA-----
Bja04 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----UGAUUCUUUGGUAUU-----
Bja05 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----AGAGCUAUCUCCACAGGCCCGGCAAGCGGCCAAA-----
Bme01 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----AGAGGGAAGAGGCAAGCCGGCAACCGGCA-----
Bme02 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----UUGCCGUGUCCUCCGAGCCGAAAGCGUCAU-----
Bme03 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----GAGCUUUGGCCCCCAU-----
Bme04 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----CGAGCCGUGUCCGUAUCCGU-----
Ccr01 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----CGAGCUUCCGUGACAU-----
Ccr02 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----GCCUGGCCCAAGGUGCGGACAAAGUUUUGCCGCACAAU-----
Cie01 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----UAAACCGCCGGCAAUCCGUGGCCAACCGGAUGCGCAAGCGGGGCUUUCAG-----
Cie02 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----CCGUGGCCCAAAUCCGGUGCGGGAACGAGUCCGUUCCGAUGA-----
Cie03 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----AUGUCCGGGACGACAGGAGGAGCUCUGCUUUUUGCGCGGUAUCGGGUGUAU-----
Cie04 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----AAAACUGGCCGUGGCAAGUAGGCCACAUAGCGCUCAAGCGCGAGCGCGGUGCAC-----
Cie05 CCGGUGCGGUGUCCCGCCGAAACUGUAA-CCGG-----

Cac01 **CCUGA** GCGGU **CCG** GCGA **CUGUA** AU **AAAGC**-----AGUUUAA GUACAAU AU-----
 Cac02 **CCAAU** GCAACCCCGUUA **CUGU** AU **ACAGUU**-----ACAAACCAAUG-----
 Cpe01 **CCGAC** GCGGU **CCG** GCGG **CUGU** AA **UAG**-----AGGAGCUUUUUGUACUUUAA-----
 Cpe02 **CUUCA** A CUACCUCA GUAA **CCGUGAA** GC-----AGACAAAUCUCAUAU-----
 Cpe03 **CCAGU** ACAGCCCCCGCUA **CUGUGAUAGG**-----AU **CA** AGUUUCUAUUUGA-----
 Cpe04 **AAU** GCAGCCCCCGCUA **CUGUUG** **AUAAG**-----GACGAGAAUAAAAG-----
 Eco01 **CUGGA** GCUGA **CGCGAG** **CGGUA** A **GGAA**-----AAGGU **CG** GAUGAUUGCGUUAUGCG-----
 Fnu01 **CCAAA** ACAGAG **CCCGUG** **CUGU** AAU **UGA**-----GUUUUUUCUUGUUUA-----
 Lig01 **CCGGA** GCUGAACCCGCA **CUGUA** A **UCGCCGA**-----AUGAUUUUCGCAUCAU-----
 Lmo01 **CCGAA** ACUGCCCCGCA **CUGU** AA **GGU**-----GGACAAGAAUCGAGAU-----
 Mlb01 **CCGUG** GCUGCCCGCA **CUGU** GU **CCGG**-----UAGUCCUCUCCAUU-----
 Mlb02 **CCGCG** GCUGUCCCGCA **CUGU** AA **CCG**-----AAGGCCAAGGCCAAAG-----
 Mlb03 **CCGCG** GCUGCCCCGCA **CGUGG** **UGGAG**-----UUCAAGUCGCAACGGGAG-----
 Mlb04 **CCGCG** GCUGCCCCGCA **CUGU** AA **CCGG**-----CGAGCCAAAGCCAUUGGU-----
 Mlb05 **CCGUG** GCUG **CCCA** AC **CUGU** AA **GGGG**-----GACCGCCCGGUAAU-----
 Mlb06 **CCGUG** GCUGCCCGCA **CUGU** AA **CCGG**-----AGAGCAAGAUCCGACA-----
 Mle01 **CCGGG** ACUGU **CCCGC** AG **CGGU** AU **CCAGG**-----AACGACCGCGUUCUGGAA-----
 Mlu01 **CCGGC** GCGGU **CCC** GCA **CUGU** CA **CCGGG**-----GAGGGA **CCCU** GUAA-----
 Mlu02 **CCGGG** ACUGU **CCCGC** AG **CGGU** AU **CCAGG**-----AACGACCGCGUUCUGGAAGUAGCAA-----
 Pae01 **CCAGC** GCUGCCCGCA **CGGU** AG **CCGA**-----AUCAGACAGCCGUGGAUGA-----
 Pae02 **CCGUG** GCUGCCCCGCA **CUGU** AU **GCAGCCUG**-----UAUUCGCGCCAUUC-----
 Pae03 **CCGGC** GCUGCCCCGCA **CGGU** AA **CCGAG**-----CGAAAUCUUCUUCAG-----

Pae04 **CCGCG**GCUGCCCGCCGCAACUGUGA**ACGG**-----CGAUCGUUCCCCAAU-----
Ppu01 **UCGGA**ACUGCCCCCGCAACUGUAG-GUGC-----CGAGCGUCUCUCCAUCGAU-----
Ppu02 **CCGGU**GCUGCCCCCGCAACGGUAA-**GCGAG**-----CGAACCUUUGAGAU-----
Ppu03 **CCGGU**GCUGCCCCCGCAACGGUAA-**GCGAG**-----UGAAGCGUGUGU-----
Ppu04 **CCCGG**GCUGCCCCCGCAACUGUAA-**GCACCG**-----ACAACGGAUCGACACA-----
Rso01 **CCUGG**GCUGCCCCCGCAACGGUAA**CGAAC**GCUGGCAAGGCCCGGCUACCUUCUGGCAGAGAGGGCGCGCGUCGCCGAGGUCCGUCCACAU-----
Sme01 **CCCGG**GCUGCCCCCGCAACGGUGG-**UGGAGC**-----GAACGCCACGGCAGAG-----
Sme02 **CCGGC**ACGUG-CCCAACCGCUGUGAA**GGG**-----GACGUUCUGGCCAAAAGGGCUCUGAAUCUUUICAGAGCUUU-----
Sme03 **UCGCA**GC CGGACCCCGCAACUGUAG**ACCGU**-----CAGGGUUCGCCAUUGGGCAUUCGCCCGGAUUTUCAACGCGCUGCAUGGGC
Sme04 **CCGUG**GCUGCCCCCGCAACUGUAA**GCGAU**-----CGUGGUUCAUCCUUGUGGGCGCAAGGCCGCA-----
Sme05 **CCGUG**GCUGCCCCCGCAACUGUGA-**GCGG**-----CGAGCAAAAGUCCAAGGAU-----
Sco01 **CCGGG**ACUGC-CCCGCA**GCGG**UGA-**GCGGG**-----AACGACCGCCGUGUA-----
Sco02 **CCGGG**ACUGU-CCCGCA**GCGG**UGA-**GUGGG**-----AACGAAAGCCGUCACA-----
Sco03 **CCGGG**ACGUUCCG-GCA**CUG**UGA-**CCGGG**-----GAGUGCACCUUGGACAC-----
Sco04 **CCCGA**ACUGU-CCCGCA**CCGUGU**-**AC**-----UUUGGUGCAUC-----
Sco05 **CCCGU**CGCGGCCUCGCCA**CUG**UGA-**ACGGG**-----AAAGCCGGCUCGGCCUGACGGGCA-----
Sri01 **CUA**GA**GCUGA**-CGCGAG**GCGG**UAA-**GGA**-----AAGGUGGAUGAUUGCGUUAUGCG-----
Som01 **CUGGC**ACUGCCCCCGCAACGGUAA**AGGU**-----GAGAGACGGCGGCAUU-----
Som02 **CCCGA**ACUGUACCGCAACUGUGA-**GUAG**-----UUAAAAGAAAGCCCUAGAUU-----
Sri01 **CCCCC**GCAGCCCCCGCUG**CUGUGAUGG**-----UGACGACCCCGUAAAGA-----
Sri02 **CUGGA**GCUGA-CGCGCA**GCGG**UAA-**GGA**-----AGGUGAGAUGAGAGCGUAAAGCA-----
Tma01 **CCGGG**GGGGG-CCCGCA**CCGUGA**-**CCGGG**-----GACGAAACCCGCAAGAAC-----
Tie01 **CCCGG**GCAGCCCCCGU**ACUGUGA**-**GGGA**-----GGACGAAAGCCCUAGUAA-----
Tie02 **CCCGG**GCAGCCCCCGU**ACUGUGA**-**GGGA**-----GGACGAAAGCCCUAGUAA-----
Vch01 **CCGGA**ACUGA-CGCGAG**GCGG**UAA-**GAGAG**-----AACGAAAGCGCUGAAAC-----
Vvu01 **CCCGA**ACUGA-CGCGAG**GCGG**UAAU**AGAG**-----AACGAAAGCUUAAUCA-----
Xac01 **CCCGA**GCUGCCCCCGCAAC**CGUGG**-**GCGAG**-----GUCAGGUGCCGCAACAG-----
Xax01 **CCCGA**GCUGCCCCCGCAAC**CGUGG**-**GCGAG**-----GUCAGAGUCCCGCACUAC-----
Ype01 **CCCGA**GCUGA-CGCGAG**GCGG**UAA**AGCGGA**-----AGUCACGGGAUAGGUUUCUAAAG-----
Aca01 **CCAGU**GCUGCCCCCGCAAC**CGGUAA**-**AAUUG**-----UAAACCAUAUUAAGAGUCAUUUAGACUUA-----

Avi01	CCGUG GCUGCCCGCCGCA CU GUUGA ACGG -----CGAGCGAUUGUCCAUCAU-----
Bfr01	CCCGG ACAGU-CCCGCUG CU UGAA GCUC -----GUCUGAAUUTC CGAUAAACAACUGUU-----
Bmg01	CCAGU ACUGCCCGCCGCA CU GUAA GUUG -----GACGAACGAGUAU-----
Lna01	CCGGU GCUGCCCCCGCA CGG UAA GGAG -----UGAAGCGUCAAU-----
Pfr01	CCCGA ACUGU-CCCGCAG CGG UCA AUGGG -----AACGACACAACGUAAG-----
Rca01	CCGCA CCCGCCCGCCGCA CCG UGAC CCGA -----GAGGGGCCCGAG-----
Rca02	CCGUG GCUGCCCGCCGCA CU GUUGA GGCG -----CGAGACGACGGUCGAAG-----
Rca03	CCGUA ACUGCCCGCCGCA CU GUAA GGCG -----CGAGCAACCCCGCGCA-----
Rsp01	CCGGC GGCGG-CCCGC CG UGUGA CGG -----GGAUGCUCGGGGCAAGAG-----
Sbi01	CCGG GCUGCCCCCGCA CGG UAA GCACGUG -----AGUCCAGGCAACAAC-----
Sgi01	CCGG ACUGC-CCCGCAG CGG UGA GU GGG-----AACGACCGCGUCAUA-----
Svi01	CCGAG ACUGCCCGCCGCA CU GUAA CCGG -----AGAGUCAUCCUCUAUGAUCGUAUCUUA ACGAUUA UA-----
Zmo01	CCUUG GCUGCCCGCCGCA CU GUAA ACAGU -----UGAAACGCCAAAAA-----
Zmo02	CCAGU GCUGCCCGCCGCA CU GUAA ACGG -----CGAGCAAAGAUCAAAAU-----

SS	Cons	ryCACUG	YGGGAAGGy
Atu01	AGC	CAAAA	UUCG
Atu02	UUCG	UUCG	UUCG
Atu03	GCUCU	GCUCU	GCUCU
Atu04	CCGG	CCGG	CCGG
Atu05	GCAA	GCAA	GCAA
Atu06	UUUAUGAUC	UUUAUGAUC	UUUAUGAUC
Bha01	UUCAU	UUCAU	UUCAU
Bha02	UACUUCU	UACUUCU	UACUUCU
Bha03	AAA	AAA	AAA
Bha04	UAGC	UAGC	UAGC
Bsu01	CAAGC	CAAGC	CAAGC
Bja01	UCCAC	UCCAC	UCCAC
Bja02	UGAC	UGAC	UGAC
Bja03	GCAA	GCAA	GCAA
Bja04	UCCUCGU	UCCUCGU	UCCUCGU
Bja05	AUCUCGG	AUCUCGG	AUCUCGG
Bme01	AAUUAU	AAUUAU	AAUUAU
Bme02	AGAU	AGAU	AGAU
Bme03	CAC	CAC	CAC
Bme04	GAAA	GAAA	GAAA
Cer01	GCUGG	GCUGG	GCUGG
Cer02	CAAAA	CAAAA	CAAAA
Cie01	GUUCA	GUUCA	GUUCA
Cie02	UCCAC	UCCAC	UCCAC
Cie03	GCCC	GCCC	GCCC
Cie04	AUAAC	AUAAC	AUAAC
Cie05	UCCAC	UCCAC	UCCAC

Cac01GAA.....GAA.....
Cac02UUUU.....GAA.....
Cpe01UAA.....GAA.....
Cpe02UUUUU.....GAA.....
Cpe03AUAAU.....GAA.....
Cpe04AAUUA.....GAA.....
Eco01AUUC.....GAA.....
Fnu01UUUU.....GAA.....
Lig01UAAAU.....GAA.....
Lmo01UUUA.....GAA.....
Mlo01UUCG.....GAA.....
Mlo02ACGUU.....GAA.....
Mlo03AAAA.....GAA.....
Mlo04GAACG.....GAA.....
Mlo05GAU.....GAA.....
Mlo06GGCA.....GAA.....
Mle01AAAA.....GAA.....
Mtu01ACA.....GAA.....
Mtu02UCAAC.....GAA.....
Pae01UCCG.....GAA.....
Pae02AUUA.....GAA.....
Pae03UCCG.....GAA.....

Pac04UGA.....GAA.....
 Ppu01CUGCC.....GAA.....
 Ppu02UCA.....GAA.....
 Ppu03UCGUAGUAC.....GAA.....
 Ppu04CAAC.....GAA.....
 Rso01CGCG.....GAA.....
 Sme01ACCGC.....GAA.....
 Sme02UUGAAGC.....GAA.....
 Sme03 AGUCUCGUAAGUUUGCGGCAUGUCGGAAAA-
UCAGCC.....UUCUUCUAC.....GCAA.....
 Sme04CGGU.....GAA.....
 Sme05AUGAAUC.....GAA.....
 Sco01ACGUAC.....GAA.....
 Sco02AUGAG.....GAA.....
 Sco03GCC.....GAA.....
 Sco04CGUACGU.....ACGUGCG--C
 Sco05CUUG.....GAA.....
 Shi01AUCC.....GAA.....
 Son01ACGAU.....GUA.....
 Son02AUU.....UAA.....
 Shi01GCAA.....GAA.....
 Shi02UCC.....GAA.....
 Tma01CGAUC.....GAA.....
 Tie01UUAGUAAAGGAGAAAAGGGGAGAGAAAU.....
 Tie02UUAGUAAAGGAGAAAAGGGGAGAGAAAU.....
 Vch01UUUCG.....GAA.....
 Vvu01GGA.....GAA.....
 Xac01ACAC.....GAA.....
 Xax01AGUC.....GAA.....
 Ype01GCAA.....GAA.....

Aca01GCAUAG.....GAA.....
Avi01CCAC.....UAA.....
Bfr01UAAA.....GAA.....
Bmg01AAAAA.....GAA.....
Lma01UCCAG.....GAA.....
Pfr01GCAA.....GAA.....
Rca01ACCA.....GAA.....
Rca02AUCCAC.....GAA.....
Rca03ACCG.....GAA.....
Rsp01UUC.....GAA.....
Sbi01ACG.....GAA.....
Sgi01GGAC.....GAA.....
Svi01UUUC.....GAA.....
Zmo01UCUA.....GAA.....
Zmo02UUUU.....GAA.....

SS >>>>>

y'y RAGYC GRAGACC GCC

Coils

Atu01 GAUAUAUUGUGAC-----CCGC-AAGUCAGGAGACCUGCCUUGAGCGGAAAUUCCACG
Atu02 GAUGAGGACGCA-----AAUCCGU--CAGCAGGAGACCUGCCGUCAAAAUUGAAACCAUCG
Atu03 UGCCGGGAAGGUGUUCAGGUUUGAC-----CCGU--AGCAGGAGACCUGCCAUACGGAAAUUCCAUGC
Atu04 GGACCAAAAGCUAUGACC-----CGC-AAGCAGGAGACCUGCCGGAUAGAUACGUCCACG
Atu05 GAAAGGGCGGATUGAA-----GCU-UAGUCAGAAAGACCCGCCUGGCAAGAUAGACCGAAC
Atu06 GGUGACAGGGUGUUGAUA-----GCCGC-AAGCAGGAGACCUGCCGUUUCAGGAAAGCGUCU
Bha01 UGUUGCAAUUGUGAC-----GCUA-CAGCAGGAGACCUGCCUGUUCUAAACAGCACUGCUU
Bha02 UUCUAAGUAGGUA-----AGCAG-CAGCAGGAGACCUGCCUUAUCCACAAGUUUCGC
Bha03 CACAUGGAGUGUGA-----UCU--AAGUCAGGAGACCUGCCUAAUGUADGCACUUGCACCC
Bha04 GCAAGUACUGCAUGAA-----CAU--AAGUCAGGAGACCUGCCUUCAGUUGAGUGUGUAG
Bsu01 -----GCCAA--GAGCAGGAUAACUCCUGUUGUUGAUCAGCACGAUU
Bja01 CGGACAGCAGCGAUGA-----CAGC--AAGCAGGAGACCGGCCCGGAGAAUUAUUGGUCCA
Bja02 GGGGAUCCAGGGCAAAACCCUG-----CUCCG-CAAGCCGGGAGACCUGCCAGCGGGACGAUUUUGGAC
Bja03 CGGAGAACCCACUGA-----ACCGC--GAGCCAGGAGACCGGCCCGUGCAUGUUUUUGAGGCCAA
Bja04 GACGAAGUGGUGACGAC-----CCGC--GAGCCAGGAGACCUGCCGUAGCCGUGGUCACACGC
Bja05 GACGUAAGGUACGAC-----CCGC--GAGCCAGGAGACCUGCCGUCAGCCGUGGUCACACGC
Bme01 GGAGGCAAGCGGAAGAG-----CCGC--AAGUCAGGAGACCUGCCGUUCCGGUACCCAUUGCU
Bme02 GCUUUAUUCGCCCAAGAC-----CCGC--GAGCAGGAGACCUGCCUGUUGCAUAGAGGCAUUGC
Bme03 GAUGGACGGCGAUUA-----UCCGC--AAGCCAGGAGACCUGCCGUGUUACGUAUCCAUUGU
Bme04 GGGUGGAAAGCGUUGA-----GCCGU--GAGCCAGGAGACCUGCCUUGAGCCGUGAACGUCCACG
Ccr01 GGGCAGGGGUGACGAC-----CCGU--GAGCCAGGAGACCUGCCUUGGACAGAUACGUCCUCC
Ccr02 GACGCCCCAGAAAGCAUUGAC-----CCGU--GAGCCAGGAGACCUGCCCGGCGCAGUCGUUUCUCCG
Cte01 CGGCAGAAUCC-----GGGA--AGUCAGAGAGACCUGCCUCAUUAUUUUUUGGCUUCGG
Cte02 UUGGAGGCGCUGAU-----GCCUGAAAGUCAGAGGAGACCUGCCUGCAUUGCAGGAGGAGGAG
Cte03 GGAAGCGA-----GGGA--GAGUCAGAAAGACCUGCCGUAUUGCAGUAAAUUGCUCC
Cte04 UGCCCGGAGGAACAGUCGAAAGUAUUUCGA-----GCCAUG--GAAGUCAGGAGACCUGCCGUAGUGGUUGGCGCCGAAU
Cte05 UGCAUCG-----AUUCAG-----CCGU--AAAGUCAGGAGACCUGCCAGUUAUCUCUUGCUCGGAA

Cac01 GUACUUAAGCA**AUGA**.....UUUUU-GAGCCAGGAUA**CUU**GCCAUUUCUAUAUGUUAUUUUU
 Cac02 UGGUUGAGGCUA.....AACUGU-GAGCCAGGAGAC**CCU**ACCUAAAAUUAUUAUGGAACUUC
 Cpe01 ACAAAAAGU**AUGA**UA.....CUU-GAGCCAGAA**GACU**GGCUAUUUUUAAACAUAAGA
 Cpe02 GAGAU**G**GAGGAAGAA.....GC-AA**UGU**CGGGAUA**CCU**GCCUUUUUAUUAA**GU**AUAUA
 Cpe03 AGAAAUGAGGAUAAG.....**CCU**UA**AGU**CAGGAUA**CCU**GCCUAAAGAUCAUGAA**CUA**AGC
 Cpe04 UUGUUUAGG**AUGA**.....UUUAU-U**AG**CAGGAG**ACU**GGCUAGUAUGCUAUU**CU**UAUUG
 Eco01 AUCAUCUCUUAAGUAUCUUA**UA**CCCC.....UCC-A**AG**CCCCGAAG**ACU**GCCGGCCACAGUCGCAUCUGGU
 Fru01 AAGAAAUUAAA.....UCA-~~UAAGCCAGAA~~AG**ACU**GCAUAAUUGAUUACUCUAUCU
 Lig01 UCGGAA.....UCCGGCA-AA**GC**CAGAA**AG**CCUAA**CA**AGUAAAAAACAACUAUA
 Lmo01 CGAUUGUUGAU**UGA**.....GCG-AA**GU**CAGGAUA**CU**GGCCAAUAAAGACGGAA**CG**AAACU
 Mio01 GGGGAAGGCGCUGAU.....CCGU-GAGCCAGGAG**ACU**GGCGAGCGGCAAAACUGACA
 Mio02 CGGCACCAAGGCG**AUG**ACC.....CGC-G**AGG**CAGGAG**ACU**GGGUCUGCGACAAAGAUCC
 Mio03 GUCGCGACCGUCCGCAAGGACA.....CUCCA-G**AGG**CCGGAA**ACA**GCCCGAGAUUUUGAACUCGAC
 Mio04 GGGCAGAGGCUU**UGA**.....CCGC-GAGCCAGGAG**ACU**GGCAGGACGAACAACGUCCACG
 Mio05 ACCGACCGGGU**UGA**.....UCCC-G**AGG**CAGAA**AG**CCGGGCUGGCAGGCAUCGUAUCCG
 Mio06 GGAUUGCGC**UGA**G**C**.....CCCG-G**AGG**CAGGAG**CCU**GCCAU**CA**CUGAGUUGACCGGAC
 Mio01 AUGGCCAUUAGAA**GC**ACCUAUCCAGUGCGCG.....CCUGG-~~GAAG~~CCGAA**AG**CCU**GC**GGGUGUGCGGGCGCGCG
 Mio01 GAGGCAAGCA**CGA**.....UCCGG-GAGCCAGGAG**ACU**GGGUGAU**CC**GGUCCUGCCACCC
 Mio02 GACGGCCAGUAGGAG**CA**CCCA**CC**GGGUGCGAG.....CCUGG-G**AG**CCGAA**AG**CCU**GC**AGCGGCGCGCGCGCG
 Pae01 GCGGCUAGAAAGCGUCCAGCGCU**U**CG.....UCCG-GAGCCCCGAG**AC**CCGGCCUG**AC**GCACCCACCGCAUCG
 Pae02 GCGCGAAAGCGGAGGUUCCUCCCCGGGUGGA**AC**GC.....CGGGCU**GG**-~~GAAG~~CAGGAG**ACU**GGCGCGAAACCAGUCGCGAGU
 Pae03 GAGGAUUCACGACC.....CUCCG-A**AG**CCCCGAG**AC**CCGGCCUG**CA**CGCCCUUGUUGGCAC

[illegible]

Avi01	GGACAAAGCCAGAC-----	CCGU--GAGCCAGGAGAGACCCUJCCCGAUAAAGCAUUGCGCAAAAGC
Bfi01	GUCGAAACAA-----	GGAGU--CAGUCAGAAGAGCCUGCCGCUUAUCAAAAGCUGUUUC
Bmg01	CUCAAGUAGAAUGA-----	UACAG--AAGUCAGGAGAGCCUGUCUUUAUUGUGAAGUUUCUUAU
Lma01	UGAUGCUIUCAAGGCCCCAGGCC-----	CUCGC--AAGCCCGGAGACCCGGCCCGAAAAAUCAGAUAAACAA
Pfi01	GUAGUGGAGGAAGUCGGGAGUGAUCUCGCAUUG-----	CCCAU--GAGUCCGAAAGACCUGCCAGGCGCGGACAAACAUUCUGUU
Rca01	GGGGCGACCGUGAGGGGACCCCCCUCGCA-----	UCCG--CAAGCCGGGAGACCUGCCAGCGCAUGGAUUUCGGGCG
Rca02	GACCCGAGUUGAUCGAA-----	CCGC--AAGUCAGGAGAGCCUGCCAUCGCUUGCGGUCGCAAG
Rca03	GGGGAGGCCACGAC-----	CCGC--AAGUCAGGAGAGCCUGCCAUCGCGUCAUACCGCC
Rsp01	GCCCCGGCGCAGAUUGAA-----	CCG--GAGCCAGAAAGACCCGCCUGACGCGAGGUAUCCCGCC
Sbi01	GCCUGGACGGUGGCCUCGCCACCC-----	GGCGGC--AAGCCGGGAGACCGGCCCGGAAGCCUCAGGUCCGGA
Sgi01	ACGGCCACUAGGUGUCUGCCCGGACAGCUG-----	CCCG--GAGUCCGAAAGACCUGCCCGCCUGCCCGCACCGACCCG
Svi01	GGAGGACCGAUAGAGAC-----	CCGC--AAGUCAGGAGACCUGCCGUAUCGAGUCACCCAUUGC
Zma01	GGUUGUUUCGAU-----	GCUGU--GAGCCAGGAGACCGACCCUAUGUAUUCGUUCCACGA
Zma02	UGAUCGACGCGGUGAC-----	CCGU--CAAGUCAGGAGACCUGCCUUAACCAAGUCAUCCACU

Consensus

D. A-Box

NC_000964.1/626134-626051 Bacillus subtilis
NC_003366.1/2870819-2870732 Clostridium perfringens
NC_004460.1/504378-504467 Vibrio vulnificus

AATTAAATAGCTATTATCACTTG-ATNA**CTCTCA**TAATATGG.**TTTGAGG**TTGCTTAC**CAGGA**.CCGTAAAT**TCCTG**.ATTACAAATTTGTTTATGACATTT
ATAAAAAAATAAATTTTGCTTCG-ATA**CTGTAA**GATATGG.**ATTAGAC**TTCTTTAC**CAGGA**.CCGAGAA.**TTCTTG**.ATTACGAAGAAAGCTTATTTCGTTT
GACTTTCGGCGATCAACGCTTTCA**TTTA****TCCTTA**TGATATNGG**TTGGGA**.TTTCTTAC**CAGAG**.CCTTAAA.**CTCTTG**.ATTATGAAGTCTGTCGCTTTATCCG

[illegible]